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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:15:36 ; Search time 33.5 Seconds
(without alignments)
1256.931 Million cell updates/sec

Title: US-09-787-126-4

Perfect score: 1675

Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPDQDNTFGAFKVDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	19 AAW83194	Human osteoprotegerin
2	1675	100.0	316	19 AAW83017	Osteoclastogenesis
3	1675	100.0	316	19 AAW59654	Amino acid sequenc
4	1675	100.0	316	20 AAY17874	Murine TRANCE. Mu
5	1675	100.0	316	21 AAY91024	Mouse OBM protein
6	1675	100.0	316	21 AAY84418	Amino acid sequenc
7	1675	100.0	316	21 AAY84419	Amino acid sequenc
8	1675	100.0	316	23 AAY78289	Mouse TRANCE prote
9	1597	95.3	318	22 AAB82092	Rat osteoclast dif
10	1554	92.8	294	19 AAW69956	NF-kB receptor act

11	1554	92.8	294	19 AAW68292	NF-kB receptor act
12	1554	92.8	294	22 AAE08737	Murine receptor ac
13	1554	92.8	294	22 AAE04425	Murine receptor ac
14	1554	92.8	294	22 AAE01992	Murine RANKL (rece
15	1417.5	84.6	317	19 AAW83195	Human osteoprotege
16	1417.5	84.6	317	19 AAW69957	NF-kB receptor act
17	1417.5	84.6	317	19 AAW68293	NF-kB receptor act
18	1417.5	84.6	317	21 AAY84417	Amino acid sequenc
19	1417.5	84.6	317	22 AAE08738	Human receptor act
20	1417.5	84.6	317	22 AAE04426	Human receptor act
21	1417.5	84.6	317	22 AAE01993	Human full-length
22	1417.5	84.6	317	23 ABB08134	Human RANKL polype
23	1417.5	84.6	317	23 AAY78285	Human TRANCE prote
24	1409.5	84.1	317	19 AAW83018	Osteoclastogenesis
25	1318	78.7	501	22 AAB84420	Amino acid sequenc
26	1297	77.4	244	19 AAW83019	A murine OCIF-bind
27	1107	66.1	246	19 AAW83020	Osteoclastogenesis
28	1101	65.7	245	20 AAY17873	Human TRANCE. Hom
29	1100	65.7	244	23 AAY86148	Human PRO206 polyp
30	1100	65.7	244	23 AAY78286	Human TRANCE prote
31	960	57.3	409	23 AAO17115	GlutathioneStransf
32	960	57.3	409	23 AAW49711	Murine GST-modf fu
33	855	51.0	160	21 AAB08272	Amino acid sequenc
34	852	50.9	173	21 AAY84421	Amino acid sequenc
35	852	50.9	187	21 AAY84420	Amino acid sequenc
36	842	50.3	173	21 AAY84422	A murine osteoprot
37	830	49.6	170	22 AAY08386	Mouse FLAG-murine
38	804.5	48.0	188	21 AAY84423	An osteoprotegerin
39	794.5	47.4	182	21 AAY84424	An osteoprotegerin
40	771	46.0	173	21 AAY84425	DNA encoding osteo
41	768	45.9	160	21 AAB08273	Amino acid sequenc
42	746	44.5	139	21 AAY91023	Mouse OBM protein
43	741	44.2	152	22 AAB67248	Human RANKL. Homo
44	732	43.7	173	21 AAY84426	An osteoprotegerin
45	387	23.1	74	21 AAY91020	Mouse OBM protein

ALIGNMENTS

RESULT 1

AAW83194

ID AAW83194 standard; Protein; 316 AA.

XX AAW83194;

AC AAW83194;

DT 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the 32D-F3 ins.

DE Human osteoprotegerin binding protein from the 32D-F3 ins.

KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
hypercalcaemia; osteoclast differentiation and activation receptor;
Paget's disease.

OS Homo sapiens.

XX W09846751-A1.

FN 22-OCT-1998.

PD 15-APR-1998; 98WO-US07584.

PF 30-MAR-1998; 98US-0052521.

XX 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

XX (AMGE-) AMGEN INC.

PA Boyle WJ;

XX WPI; 1998-594578/50.

PI N-PSDB; AAV70284.

DR

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 XX
 PS Claim 19; Fig 1; 47pp; English.
 XX
 CC The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (OAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 SQ Sequence 316 AA;

Query Match 100.0%; Score 1675; DB 19; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKYLRSSEMGSGVPEHPLHPAPSAPAPPPAASRSMFLALLGLGLQ 60
 DB 1 MRRASRDYKYLRSSEMGSGVPEHPLHPAPSAPAPPPAASRSMFLALLGLGLQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISDSTHCYRILRLHENAGLDSTLESDTLPDSCRMMQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISDSTHCYRILRLHENAGLDSTLESDTLPDSCRMMQ 120
 QY 121 AFGAVQKELQHVGPQRFSGAPAMMEGSLDVAQKPEAQPFAHLTINAASIPSGSHK 180
 DB 121 AFGAVQKELQHVGPQRFSGAPAMMEGSLDVAQKPEAQPFAHLTINAASIPSGSHK 180
 QY 181 VTLSWYHGRGWAQKISNMTLSNGLKRVNDGFFYLYANICFRHETSGSVPTDYQLQMY 240
 DB 181 VTLSWYHGRGWAQKISNMTLSNGLKRVNDGFFYLYANICFRHETSGSVPTDYQLQMY 240
 QY 241 VKTISKIPSSHNLKMGSGTKNWSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
 DB 241 VKTISKIPSSHNLKMGSGTKNWSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300
 QY 301 DQDATYFGAFKVDID 316
 DB 301 DQDATYFGAFKVDID 316

RESULT 2
 AAW83017
 ID AAW83017 standard; Protein; 316 AA.
 AC
 XX
 AC AAW83017;
 XX
 DT 10-FEB-1999 (first entry)
 DE
 XX Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism.
 XX
 OS Unidentified.
 XX

PN WO9846644-A1.

XX 22-OCT-1998.

XX 15-APR-1998; 98WO-JP01728.

XX 02-DEC-1997; 97JP-0332241.

XX 15-APR-1997; 97JP-0097808.

XX 09-JUN-1997; 97JP-0151434.

XX 12-AUG-1997; 97JP-0217897.

XX 21-AUG-1997; 97JP-0224803.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kinoshita M, Kobayashi E, Morinaga T;

XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;

XX Washida N, Yamaguchi K, Yano K, Yasuda H;

XX WPI; 1998-594563/50.

XX N-PSDB; NAW69886.

XX protein binding to osteoclastogenesis inhibitory factor - useful

XX for, e.g. treatment and investigation of disorders of bone and

XX calcium metabolism

XX Claim 8; Pages 106-108; 151pp; Japanese.

XX The present sequence represents an osteoclastogenesis inhibitory factor

XX (OCIF)-binding molecule (OBM). The protein promotes and supports the

XX separation and maturation of osteoclasts in the presence of bone

XX absorption factors such as calcitriol or parathyroid hormone (PTH).

XX OBM is isolated from stroma cells cultured in the presence of a bone

XX absorption factor by separation and solubilisation of membrane proteins

XX then affinity chromatography using OCIF. It exists in a full-sequence

XX form and a solubilised form (SOBM) which is a shorter chain. OBM may be

XX used for screening potential inhibitors and modifiers of its biological

XX activity, and screening for receptors to OBM which mediate its function.

XX These substances can then be used in the treatment of disorders of bone

XX function and calcium metabolism. The antibodies can be used for assay

XX of the protein, for investigative and diagnostic purposes, and as

XX components of drugs.

XX Sequence 316 AA;

Query Match 100.0%; Score 1675; DB 19; Length 316;

Best Local Similarity 100.0%; Pred. No. 2.6e-143;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYKYLRSSEMGSGVPEHPLHPAPSAPAPPPAASRSMFLALLGLGLQ 60

DB 1 MRRASRDYKYLRSSEMGSGVPEHPLHPAPSAPAPPPAASRSMFLALLGLGLQ 60

QY 61 VVCSIALFLYFRAQMDPNRISDSTHCYRILRLHENAGLDSTLESDTLPDSCRMMQ 120

DB 61 VVCSIALFLYFRAQMDPNRISDSTHCYRILRLHENAGLDSTLESDTLPDSCRMMQ 120

QY 121 AFGAVQKELQHVGPQRFSGAPAMMEGSLDVAQKPEAQPFAHLTINAASIPSGSHK 180

DB 121 AFGAVQKELQHVGPQRFSGAPAMMEGSLDVAQKPEAQPFAHLTINAASIPSGSHK 180

QY 181 VTLSWYHGRGWAQKISNMTLSNGLKRVNDGFFYLYANICFRHETSGSVPTDYQLQMY 240

DB 181 VTLSWYHGRGWAQKISNMTLSNGLKRVNDGFFYLYANICFRHETSGSVPTDYQLQMY 240

QY 241 VKTISKIPSSHNLKMGSGTKNWSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300

DB 241 VKTISKIPSSHNLKMGSGTKNWSNPFHYSINVGFFKLRAGEEISIQVSNPSLLDP 300

QY 301 DQDATYFGAFKVDID 316

DB 301 DQDATYFGAFKVDID 316

RESULT 3

AAW59654
ID AAW59654 standard; Protein; 316 AA.

XX AC AAW59654;

XX DT 24-SEP-1998 (first entry)

XX DE Amino acid sequence of mouse 499E9 protein.

XX KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
XX KW antagonist; autoimmune disorder; rheumatoid arthritis;
XX KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
XX KW acute inflammatory response; antibody; antigen; cancer.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX DT 1..49

XX FT Domain /note= "intracellular domain"

XX FT 70..316

XX FT Domain /note= "extracellular domain"

XX PN W09825958-A2.

XX PD 18-JUN-1998.

XX PF 12-DEC-1997; 97WO-US22766.

XX PR 13-DEC-1996; 96US-0032846.

XX FA (SCHE) SCHERING CORP.

XX PI Gorman DM, Mattson JD;

XX DR WPI: 1998-348452/30.

XX DR N-PSDB; AAW41489.

XX FT Mouse cell surface antigen, 499E9 protein - used to treat conditions
XX FT associated with abnormal physiology or development

XX PS Claim 1; Pages 8-11; 59pp; English.

XX CC This is the amino acid sequence of the mouse 499E9 protein, used
XX CC in the method of the invention to treat conditions associated with
XX CC abnormal physiology or development. The 499E9 protein is expressed
XX CC highly on polarised Th1 T cells, binding of 499E9 to its receptor may
XX CC result in either immune cell expansion or apoptosis. Antagonists of
XX CC 499E9 may be used to modulate immune responses in abnormal situations,
XX CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
XX CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
XX CC acute inflammatory responses in which T-cell expansion, activation or
XX CC immunological T-cell memory play an important role. The antibodies
XX CC can be used to raise anti-idiotypic antibodies which will be useful
XX CC in detecting or diagnosing various immunological conditions related to
XX CC the expression of antigens of 499E9. The antibodies, and fragments of
XX CC 499E9 can be used in the treatment of conditions associated with
XX CC abnormal physiology or development, including abnormal proliferation
XX CC (e.g. cancerous conditions) or degenerative conditions.

XX SQ Sequence 316 AA;

Query Match

Best Local Similarity 100.0%; Score 1675; DB 19; Length 316;

Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYGYKLRSEFGSGVPHGGLHPAPCAPAPPAPPAASRSMFALLGLGIGQ 60

DB 1 MRRASRDYGYKLRSEFGSGVPHGGLHPAPCAPAPPAPPAASRSMFALLGLGIGQ 60

QY 61 VVCSTALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120

DB 61 VVCSTALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQ 120

QY 121 AFOGAVOKELQHLVGPORFSGAPAMMEGSLDVAORCKPEAOPFAHLTINAAISPSGSHK 180
DB 121 AFOGAVOKELQHLVGPORFSGAPAMMEGSLDVAORCKPEAOPFAHLTINAAISPSGSHK 180
QY 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLQLMVY 240
DB 181 VTLSWYHDRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLQLMVY 240
QY 241 VVTSIKIPSSHNLKMGSTKNSGNSSEFHFYSINVGGFKLKLRAGEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSSHNLKMGSTKNSGNSSEFHFYSINVGGFKLKLRAGEISIQVSNPSLLDP 300
QY 301 DQDATYFGAFKVDID 316
DB 301 DQDATYFGAFKVDID 316

RESULT 4

AAW17874

ID AAW17874 standard; Protein; 316 AA.

XX AC AAW17874;

XX DT 17-AUG-1999 (first entry)

XX DE Murine TRANCE.

XX KW TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
XX KW TNF-related activation induced cytokine; immune response; cancer;
XX KW autoimmune disease; HIV; hypersensitivity; allergen.

XX OS Mus musculus.

XX PN W09929865-A2.

XX PD 17-JUN-1999.

XX PF 14-DEC-1998; 98WO-US26486.

XX PR 11-DEC-1998; 98US-0989479.

XX PR 12-DEC-1997; 97US-0989479.

XX PR 03-MAR-1998; 98US-0034099.

XX FA (UYRQ) UNIV ROCKEFELLER.

XX PI Choi Y, Josien R, Steinman R, Won B;

XX DR WPI: 1999-385609/32.

XX DR N-PSDB; AAX80224.

XX FT TNF like proteins for treating autoimmunity and cancer

XX PS Claim 9; Fig 3; 164pp; English.

XX CC The present sequence represents murine TRANCE-related activation induced
XX CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX CC variants, fragments, derivatives or analogues may be used as modulators
XX CC of immune response in a mammal comprising, antisense sequences to
XX CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX CC Agonists and antagonists of TRANCE, can be used to modulate immune
XX CC response by increasing or decreasing the life span of mature dendritic
XX CC cells and increasing or decreasing T cell activation. These techniques
XX CC are especially useful for treating immune system related conditions such
XX CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX CC The TRANCE polypeptides can be used to increase the viability of
XX CC dendritic cells in vivo or in vitro, especially when used in conjunction
XX CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CC CD40L or TNF-alpha).

XX SQ Sequence 316 AA;

Query Match

100.0%; Score 1675; DB 20; Length 316;

PN XX
XX XX
PD PD
XX XX
XX XX
PF PF
XX XX
13-SEP-1999; 99WO-DK00481.
XX XX
15-SEP-1998; 98DK-0001164.
PR PR
02-OCT-1998; 98US-0102896.
XX XX
XX XX
(MEBI-) M & E BIOTECH AS.
PA PA

1;

QY 1 MRRASRDYGYKLSRSEMGSGVPGHPLPAPAPAPPPAASRSMFLALGLGLGQ 60
 DB 1 MRRANRDYGYKLSRSEMGSGVPGHPLPAPAPAPPPAASRSMFLALGLGLGQ 60
 QY 61 VVCSIALFLYFRQADPNRISSESTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 118
 DB 61 VVCSIALFLYFRQADPNRISSESTHCFYRILRLHENAGLQDSTLESDTLEALPDSCRRM 120
 QY 119 KOAFQAVQKELQHVGPQRFSGAPAMEGSWLDVAQRGKPEAQPFAHLTINAAISPSGS 178
 DB 121 KOAFQAVQKELQHVGPQRFSGVPAAMEGSWLDVAQRGKPEAQPFAHLTINAAISPSGS 180
 QY 179 HKVTLSSWYHNRGWAKISNMTLSNGKLRVNDGFFYILYANICFRHHETSGVPTDYQLQM 238
 DB 181 HKVTLSSWYHNRGWAKISNMTLSNGKLRVNDGFFYILYANICFRHHETSGVPTDYQLQM 240
 QY 239 VYVYKTSIKIPSSHNLMKGGSTRNWSNSEFHYTSINVGFFFKLRAGEEISIQVSNPSSL 298
 DB 241 VYVYKTSIKIPSSHNLMKGGSTRNWSNSEFHYTSINVGFFFKLRAGEEISIQVSNPSSL 300
 QY 299 DPQDQATYFGAFKVDID 316
 DB 301 DPQDQATYFGAFKVDID 318

RESULT 10

AAW69956
 ID AAW69956 standard; Protein: 294 AA.

XX AC AAW69956;

XX DT 08-OCT-1998 (first entry)

XX DE NF-kB receptor activator RANK ligand (RANKL).

XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX OS Mus musculus.

XX PN WO9828426-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23775.

XX R 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX XX 07-MAR-1997; 97US-0813509.

XX PA (IMMV) IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX DR WPI; 1998-377657/32.

XX DR N-PSDB; AAV41371.

XX PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells

XX PS Claim 27; Pages 55-57; 80pp; English.

XX CC This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an

CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

XX SQ Sequence 294 AA;

Query Match 92.88; Score 1594; DB 19; Length 294;

Best Local Similarity 99.7%; Pred. No. 2,1e-132;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGPHLPAPAPAPPPAASRSMFLALGLGLGQVVCISIALFLYFRQADPNRISE 82

DB 1 GVPHEGPHLPAPAPAPPPAASRSMFLALGLGLGQVVCISIALFLYFRQADPNRISE 60

QY 83 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMQAFOGAVQKELQHVGPQRFSGA 142

DB 61 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMQAFOGAVQKELQHVGPQRFSGA 120

QY 143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAAISPSGSHKVTLSSTHNRGWAKISNMTLSN 202

DB 121 PAMMEGSWLDVAQRGKPEAQPFAHLTINAAISPSGSHKVTLSSTHNRGWAKISNMTLSN 180

QY 203 GLKRVNDGFFYILYANICFRHHETSGSVPTDYQLQMVTYVVKTSIKIPSSHNLMKGGSTKN 262

DB 181 GLKRVNDGFFYILYANICFRHHETSGSVPTDYQLQMVTYVVKTSIKIPSSHNLMKGGSTKN 240

QY 263 WSGNSEFHYTSINVGFFFKLRAGEEISIQVSNPSSLDPDQDQATYFGAFKVDID 316

DB 241 WSGNSEFHYTSINVGFFFKLRAGEEISIQVSNPSSLDPDQDQATYFGAFKVDID 294

RESULT 11

AAW68292

ID AAW68292 standard; Protein: 294 AA.

XX AC AAW68292;

XX DT 08-OCT-1998 (first entry)

XX DE NF-kB receptor activator RANK ligand (RANKL).

XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX OS Mus musculus.

XX PN WO9828426-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23866.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX PA (IMMV) IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX DR WPI; 1998-377655/32.

XX DR N-PSDB; AAV41371.

XX PT New isolated receptor activator of necrosis factor-kappa B - useful

1. *Phragmites australis* (Cav.) Trin. ex Steud.

QY	23	GYPHEGFLPAPSA	PAPAPPPPAAS	RSFMFLALIGL	IGVGVCSIALFLY	FFRAQMDPNRISE	82
Db	1	GYPHEGFLPAPSA	PAPAPPPPAAS	RSFMFLALIGL	IGVGVCSIALFLY	FFRAQMDPNRISE	60
QY	83	DSTHCFYRILRL	UHENAGLDSTL	SEEDTLPS	CDSCRMRKQAF	OGAVOKELQHI	TVGPQPSGA 1424
Db	61	DSTHCFYRILRL	UHENADQDSTL	SEEDTLPS	CDSCRMRKQAF	OGAVOKELQHI	TVGPQPSGA 1204
QY	143	PAMMEGSWLDV	AQRKPEAQPAH	LITINAA	SIPSGSHKVTLS	SSYHDRGWAKIS	NTMTLSN 2024
Db	121	PAMMEGSWLDV	AQRKPEAQPAH	LITINAA	SIPSGSHKVTLS	SSYHDRGWAKIS	NTMTLSN 1804
QY	203	GKLRVNODGFY	LIYANICPRH	HETSGSVPTDY	LQLMVYVVKTS	IKIPSSHNLKMG	GSTKN 2624
Db	181	GKLRVNODGFY	LIYANICPRH	HETSGSVPTDY	LQLMVYVVKTS	IKIPSSHNLKMG	GSTKN 2404

QY 263 WSGNSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 316
 Db 241 WSGNSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 294

RESULT 13
 AAE04425
 ID AAE04425 standard; Protein; 294 AA.
 XX AC AAE04425;
 XX DT 04-SEP-2001 (first entry)
 XX DE Murine receptor activator of NF- χ 1 B ligand (RANKL) protein.
 XX KW Murine; receptor activator of NF- χ 1 B; RANK; tumour necrosis factor;
 KW CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
 W chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
 JS Mus musculus.

XX Key Location/Qualifiers
 FH Region 139..294
 FT /note="Receptor binding region"
 XX US6242213-B1.
 XX 05-JUN-2001.
 XX 22-DEC-1997; 97US-0995659.
 XX 23-DEC-1996; 96US-0059978.
 PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 XX (IMMV) IMMUNEX CORP.
 XX PA Anderson DM;
 XX PI WPI; 2001-407216/43.
 DR N-PSDB; AAD08714.
 XX New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF- χ 1 B
 PT receptor activator) of the receptor activator of NF- χ 1 B (RANK)
 XX Example 7; Column 59-62; 43pp; English.

CC The present invention relates to receptor activator of NF- χ 1 B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumour necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
 CC The ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is murine RANKL protein.
 XX Sequence 294 AA;

Query Match 92.88; Score 1554; DB 22; Length 294;
 Best Local Similarity 99.78; Pred. No. 2.le-132;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPAPAPAPAPAPASRSMFLALIGLIGQVCSIALFLYFRAQMDPNRISE 82
 Db 1 GVPHEGLHPAPAPAPAPAPAPASRSMFLALIGLIGQVCSIALFLYFRAQMDPNRISE 60
 QY 83 DSTHCFYRILRHENAGLDSTLESDTLPSDCRRMKQAFQVQKELQHLIVGQPFSGA 142
 Db 61 DSTHCFYRILRHENAGLDSTLESDTLPSDCRRMKQAFQVQKELQHLIVGQPFSGA 120

QY 143 PAMEGSWLDVAQRKPEAQPFHAHTINAASIPSGSHKVTLSWYHDSGWAKISNWTLSN 202
 Db 121 PAMEGSWLDVAQRKPEAQPFHAHTINAASIPSGSHKVTLSWYHDSGWAKISNWTLSN 180
 QY 203 GKLRVNDGFFYLYANICFRHETSGSVPTDYQLQMVVYVTKSIKIPSSHNLKMGSGTKN 262
 Db 181 GKLRVNDGFFYLYANICFRHETSGSVPTDYQLQMVVYVTKSIKIPSSHNLKMGSGTKN 240
 QY 263 WSGNSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 316
 Db 241 WSGNSEPHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYGAFAKVDID 294

RESULT 14
 AAE01992
 ID AAE01992 standard; Protein; 294 AA.
 XX AC AAE01992;
 XX DT 31-JUL-2001 (first entry)
 XX DE Murine RANKL (receptor activator of NF-kappaB ligand) protein.
 XX KW Mouse; receptor activator of NF-kappaB; RANK; nuclear factor-kappaB;
 KW NF-kappaB; tumour necrosis factor; TNF; type I transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopathic;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 XX early onset Paget's disease of bone; EP; cytostatic.
 XX OS Mus musculus.
 XX WO200136637-A1.
 XX 25-MAY-2001.
 XX 14-NOV-2000; 2000WO-US31459.
 XX 17-NOV-1999; 99US-0442029.
 XX (IMMV) IMMUNEX CORP.
 XX PA Anderson DM, Hughes AE;
 XX WPI; 2001-329222/34.
 DR N-PSDB; AAD05903.
 XX New DNA encoding a receptor activator of NF-kappaB polypeptide for the
 PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 PT Disclosure; Page 74-75; 96pp; English.

XX The present invention relates to a novel receptor, referred to as RANK
 CC (receptor activator of NF (nuclear factor)-kappaB), a member of TNF
 CC (tumour necrosis factor) receptor superfamily. RANK is a type I
 CC transmembrane protein that interacts with TNF receptor-associated
 CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
 CC of RANK and membrane bound NF-kappaB (RANKL) results in upregulation
 CC of the transcription factor NF-kappaB, a ubiquitous transcription factor
 CC that is most extensively utilised in cells of the immune system.
 CC Inhibition of NF-kappaB by RANK antagonists is useful in ameliorating
 CC negative effects of inflammatory reactions, and the effects of excess
 CC bone resorption. The RANK DNAs, proteins and their analogues are useful
 CC for the preparation of pharmaceutical compositions, for infecting target
 CC cells for use in gene therapy applications in diagnosing diseases
 CC associated with RANK, and as targets for use in screening assays. They
 CC may be used in the treatment or diagnosis of immune system dysfunction.
 CC The present invention also encompasses gene therapy methods to correct
 CC gene-activating mutations, associated with e.g. familial expansile
 CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 CC present amino acid sequence is murine RANKL (murRANKL) protein.
 XX Sequence 294 AA;

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OM protein - protein search, using sw model.

Run on: April 16, 2003, 12:17:02 ; Search time 15.5 Seconds
(without alignments)
1959.902 Million cell updates/sec

Title: US-09-787-126-4
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSSEMGs.....LLDPDQDVFAGKQVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185.5	11.1	261	2 S53090	CD40 ligand - bovi
2	183	10.9	278	2 A49266	Fas ligand - rat
3	182	10.9	279	2 A53062	Fas ligand - mouse
4	173.5	10.4	281	2 T38707	Fas ligand - human
5	171.5	10.2	261	2 T53476	CD40 ligand - huma
6	157	9.4	260	2 S21738	CD40 ligand - mous
7	149	8.9	234	1 J01344	tumor necrosis fac
8	146.5	8.7	235	1 QMNSN	tumor necrosis fac
9	143.5	8.6	233	1 S22052	tumor necrosis fac
10	141	8.4	234	1 JH0529	tumor necrosis fac
11	140	8.4	233	2 S11688	tumor necrosis fac
12	139.5	8.3	233	1 QWHUN	tumor necrosis fac
13	137.5	8.2	234	1 A25451	tumor necrosis fac
14	135.5	8.1	235	2 S154490	tumor necrosis fac
15	133.5	8.0	233	1 S24642	tumor necrosis fac
16	133	7.9	185	2 S52715	tumor necrosis fac
17	133	7.9	232	1 S12606	tumor necrosis fac
18	129.5	7.7	235	2 JH0029	tumor necrosis fac
19	129.5	7.7	306	2 T49139	lymphotoxin-beta
20	117	7.0	244	2 A46066	lymphotoxin beta
21	115.5	6.9	193	2 S06192	tumor necrosis fac
22	103.5	6.2	340	2 S49742	hypothetical prote
23	103	6.1	3848	2 T17414	TipC protein - ali
24	99.5	5.9	558	2 T23649	hypothetical prote
25	99	5.9	440	2 T49681	glyceraldehyde-3-p
26	97	5.8	450	2 S38114	hypothetical prote
27	95.5	5.7	553	2 B55514	dihydrolipoamide S
28	94	5.6	1486	1 B40333	collagen alpha 1(I
29	93.5	5.6	205	1 QWHDX	lymphotoxin alpha

30	92.5	5.5	197	1 JH0309	tumor necrosis fac
31	92	5.5	549	2 JC5926	secreted klotho pr
32	92	5.5	785	2 T23456	hypothetical prote
33	92	5.5	1012	2 JC5925	membrane klotho pr
34	90.5	5.4	658	2 T39500	serine/threonine-s
35	90.5	5.4	750	2 E84475	probable Athila re
36	90.5	5.4	952	2 AC0447	probable insectici
37	90	5.4	3011	1 S40770	genome polyprotein
38	89	5.3	1694	2 S50065	stalladhesin - mou
39	88.5	5.3	202	1 E27303	tumor necrosis fac
40	88.5	5.3	477	2 T38409	adenyl cyclase-a
41	88.5	5.3	1547	2 J00096	hypothetical 178k
42	88	5.3	347	2 H75253	hypothetical prote
43	88	5.3	560	1 J01221	probable 60K inner
44	88	5.3	1420	2 T37781	probable cytoskele
45	88	5.3	2774	2 A43359	microtubule-associ

ALIGNMENTS

RESULT 1

S53090
CD40 ligand - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C:Accession: S53090
R:Mertens, B.E.L.C.; Muriuki, M.
A:Submitted to the EMBL Data Library, February 1995
A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A:Reference number: S53090
A:Accession: S53090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <MER>
A:Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match 11.1%; Score 185.5; DB 2; Length 261;
Best Local Similarity 25.1%; Pred. No. 5.4e-08;
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;

Qy	32	PAPSAPAPPPAASRSRSMFLALLGLGQVVCSTIALF-LYFRAQMDPNRISDSTHCFTYR	90
Db	8	PSRSVANGPP-VSMKIFVLLTVFLITQMTGSAFVYLHRLD--KIEDER-----	57
Qy	91	ILRLHE-----NAGLDSTLESIEDYLPDSCRMKAPQAGAVOKELQHVGPQR	139
Db	58	--NLHEDFVFMKTIQRCNKEGSLSL-----NCEIRSRFEDLVKDIMON-----	104
Qy	140	SGAPAMEGSWLDVAQRGKPEAQPFAHLTINAASTPSGSHKVTLSSTWYHRCWAKISN--	197
Db	105	KKKENFE-----MHKGDEPQIAAHV-----ISEASSTTSVLQWAPRGTYVLSNML	152
Qy	198	MTLSNGK-LRYNQDGFYLYANICF-RHETSGSVPTDYQLQWTVVTKTSIKIPSSH--	253
Db	153	VTLENGKQLAVKRGFYIYITQVTCNSRNETLSQAP-----FIASCLAKSPSGSRI	204
Qy	254	LMKGSTKNWGSNEFHYSINVGFFKLRAGEEISIQVSNPSLDDPDODATYFGAFKV	312
Db	205	LLRAANTH--SSSKPCGOQSILHGVFELQSGAVFVNVTPDPSQVSHGTGFTSGLLKL	261

RESULT 2

A49266
Fas ligand - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: A49266
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
A:Cell 75, 1169-1178, 1993
A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the
A:Reference number: A49266; MUID:94084792; PMID:7505205
A:Accession: A49266

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <SUD>
A:Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C:Keywords: glycoprotein; transmembrane protein

Query Match 10.9%; Score 183; DB 2; Length 278;
Best Local Similarity 23.4%; Pred. No. 9.5e-08;
Matches 75; Conservative 42; Mismatches 107; Indels 96; Gaps 13;

QY 14 SSEEMSG-----PGVPHEGLHPAPSAPAPP-----PAASRSMFLAL 54
DB 34 SSGPRGQRRPPPPPPSPL-PPPSQPPPLPLPLKKNIELWLVFFPMVLV 92
QY 55 GLIGQVVCVIALFLYRAQMDNRISEDTHCFYRILRLHENAGLDQSTLESEDILPDS 114
DB 93 GMGLG-----MYQLFHLQKELAELEFTH-----SLRVSSFEKQIANPST 133
QY 115 CRMKQAFQAVOKELQHIYVGPORFSGAPAMGSLDVAQRKPEAQPPAHLTIN-AA 172
DB 134 PSETK-----KPRS--VAHLTGPNRPR 153
QY 173 SIPSGSHKVTLSWYHGRGAKISNMTLSNGKLRVNDGCFYILYANICFRHHETSGSVPT 232
DB 154 SIP-----LEWEDTYGTALISGVKYGKGLVINEAGLYFYYSKYPR-GQSCNSQP- 203
QY 233 DYQLQVMVVKTSIKIPSSHNLMKGGSTKNWGSNPFYYSINVGFFKLRAGEEISIOV 292
DB 204 --LSHKVYM--RNFKPGDVLVME-EKRLNYCTTGQIWAHSSYLGAENLTVADHLXVNI 258
QY 293 SNPSLLDPQDATYFGAFKY 312
DB 259 SOLSLINFESKTFFGLYKL 278

RESULT 3

Fas ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
R:Accession: A53062
R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag
Cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in
A:Reference number: A53062; MUID:94185175; PMID:7511063
A:Accession: A53062
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TAK>
A:Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.9%; Score 182; DB 2; Length 279;
Best Local Similarity 22.7%; Pred. No. 1.2e-07;
Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;

QY 13 RSSEEMSGGVPHEGLHPAPSAPAPP-----PAASRSMFLALIGL 57
DB 38 RGPDRPPPPPPVPSPL-PPPSQPPPLPLPLKKNHNTNLWLVVFFPMVLVAGVG 96
QY 58 LGQVVCVIALFLYRAQMDNRISEDTHCFYRILRLHENAGLDQSTLESEDILPDCRR 117
DB 97 LG-----MYQLFHLQKELAE-----LREFTNLSKVSFEKQIANPST--- 134
QY 118 MKQAFQAVOKELQHIYVGPORFSGAPAMGSLDVAQRKPEAQPPAHLTIN--AASIP 175
DB 135 -----PSE-----KKEPRVAHLTGPHRSRIP 157
QY 176 SGSEKVTLSWYHGRGAKISNMTLSNGKLRVNDGCFYILYANICFRHHETSGSVPTDY 235
DB 158 -----LEWEDTYGTALISGVKYGKGLVINEAGLYFYYSKYPR-GQSCNNQPLNH- 207
QY 236 QLVAVVVKTSIKIPSSHNLMKGGSTKNWGSNPFYYSINVGFFKLRAGEEISIOVSNP 295

DB 208 --KVYM--RNSKYPEDVLVME-EKRLNYCTTGQIWAHSSYLGAENLTVADHLXVNI 262
QY 296 SILDPDQDATYFGAFKY 312
DB 263 SLINFESKTFFGLYKL 279

RESULT 4

Fas ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
R:Accession: I38707; JC2340; S57565; I38554
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A:Title: Human Fas ligand: gene structure, chromosomal location and species specifi
A:Reference number: I38707; MUID:95127560; PMID:7826947
A:Accession: I38707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-281 <RES>
A:Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431
R:Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusanoto
Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A:Reference number: JC2340; MUID:95071350; PMID:7980502
A:Accession: JC2340
A:Molecule type: DNA
A:Residues: 1-281 <MIT>
A:Cross-references: GB:D38122; DBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g1361
R:Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A:Reference number: S57565
A:Accession: S57565
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-281 <SCH>
A:Cross-references: EMBL:X89102; NID:g887455; PID:g887456
R:Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.
J. Exp. Med. 181, 71-77, 1995
A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A:Reference number: I38554; MUID:95105731; PMID:7528780
A:Accession: I38554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-281 <RE2>
A:Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628
C:Genetics:
A:Gene: FasL
A:Introns: 151/1; 116/3
C:Keywords: glycoprotein; transmembrane protein
F:80-102/Domain: transmembrane #status predicted <TMM>
F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 173.5; DB 2; Length 281;
Best Local Similarity 21.2%; Pred. No. 6e-07;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps 9;

QY 22 PGVPHEGLHPAPSAPAPPAPASR-----SMFLALIGL 58
DB 40 PGQRPPPPPPPPPPPPPPPPPPPLPLPLPKKGNHSTGLCLLVNFFMVLVGLGL 99
QY 59 GOVVCVIALFLYRAQMDNRISEDTHCFYRILRLHENAGLDQSTLESEDILPDCRRM 118
DB 100 G-----MYQLFHLQ-----KELAELESTSQHHTA----- 124
QY 119 KQAFQAVOKELQHIYVGPORFSGAPAMGSLDVAQRKPEAQPPAHLT--INAAISIP 176
DB 125 -----SSLEKQIGHPSPPPE-----KKELRKVAHLTGKNSRSM- 159
QY 177 GSHKVTLSWYHGRGAKISNMTLSNGKLRVNDGCFYILYANICFRHHETSGSVPTDY 236
DB 160 -----LEWEDTYGTALISGVKYGKGLVINEAGLYFYYSKYPRGQSCNN-----LP 206

QY 237 LMVYVVKTSIKIPSSNLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVNSPS 296
 Db 207 LSKHYVTRNSKYPQDILVME-GROMSYCTGOMWARSYLIGAVNLTSDHLVYVNSLS 265
 QY 297 LLDPDQDATYFGAFKV 312
 Db 266 LVNFESQTFEGLYKL 281

RESULT 5

CD40 ligand - human
 N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
 C:Species: Homo sapiens (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
 C:Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
 R: Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
 MBO J. 11, 4313-4321, 1992
 A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
 A:Reference number: S28017; MUID:93049181; PMID:1385114
 A:Accession: S28017
 A:Molecule type: mRNA
 A:Residues: 1-261 <HOL>
 A:Cross-references: EMBL:Z15017; NID:938483; PIDN:CAA78737.1; PID:938484
 R: Spriggs, M.K.; Armitage, R.J.; Stockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
 J. Exp. Med. 176, 1543-1550, 1992
 A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
 A:Reference number: JH0793; MUID:93094757; PMID:1281209
 A:Accession: JH0793
 A:Molecule type: mRNA
 A:Residues: 1-261 <SPB>
 A:Cross-references: GB:X67878; NID:938411; PIDN:CAA48077.1; PID:938412
 R: Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.
 Eur. J. Immunol. 22, 3191-3194, 1992
 A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A:Reference number: S26694; MUID:93076854; PMID:1280226
 A:Accession: S26694
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-261 <GRA>
 A:Cross-references: EMBL:X68550; NID:937269; PIDN:CAA48554.1; PID:937270
 R: Gauchat, J.F.; Aubry, J.P.; Marzel, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
 FEBS Lett. 315, 259-266, 1993
 A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
 A:Reference number: S28852; MUID:93138085; PMID:7678552
 A:Accession: S28852
 A:Molecule type: mRNA
 A:Residues: 1-261 <GAU>
 A:Cross-references: EMBL:L07414; NID:9180123; PIDN:AAA35662.1; PID:9180124
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
 C:Genetics:
 A:Gene: GDB:CD40LG; HIGM1; IMD3
 A:Cross-references: GDB:120632; OMIM:308230
 A:Map position: Xq26-Xq26
 C:Keywords: glycoprotein; transmembrane protein
 F:13-44/Domain: transmembrane #status predicted <TMM>
 F:45-261/Domain: extracellular #status predicted <EXT>
 F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.28; Score 171.5; DB 2; Length 261;
 Best Local Similarity 25.28; Pred. No. 8e-07;
 Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

QY 33 APSAPAPAPPAASRSMFLALLIGIGVVCYSIALF-LYFRAQMDPNRISEDSHCFYRI 91
 Db 9 SPSSAATGLP--ISMKIFMVLITVFLITQMGSAFVLYLHRLD--KIEDER----- 57
 QY 92 LRLHE-----NAGLDQSTLESDTLPDSCRMKQAFQAGVQKELQHVGPORFS 140
 Db 58 -NLHEDFVFNKTIQRCNTGERSLSLL-----NCEIKSQFEGFV-KDIM-----LN 101

QY 141 GAPAMGSLDVAORKEPAQFAHLTINAAISPSGSHKVTLSWYHGRWAKISN--M 198
 Db 102 KEETKENSF--EMKGDONPOLAAHV-----ISASSTTSVLQWAEKGYTMMNLV 153
 QY 199 TISNGK-LRVNODGFYLYANICF-RHETSGSVPTDYQLQVMVYVVKTSIKIPSSN--L 254
 Db 154 TLENGKQLTVKROGLYIYAQVTFCSNREASSQAP-----FIASLCLKSPGFERIL 205
 QY 255 MKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVNSPSLLDPDQDATYFGAFKV 312
 Db 206 LRAANTH--SSAKPCQGSIHLLGVFELOPGASVFVNVDPSQVSHGTGFTSFGLLKL 261

RESULT 6

S21738
 CD40 ligand - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C:Accession: S21738
 R: Armitage, R.J.; Fänslow, W.C.; Stockbine, L.; Sato, T.A.; Clifford, K.N.; Macdu
 ; Cosman, D.; Spriggs, M.K.
 Nature 357, 80-82, 1992
 A:Title: Molecular and biological characterization of a murine ligand for CD40.
 A:Reference number: S21738; MUID:92244364; PMID:1374165
 A:Accession: S21738
 A:Molecule type: mRNA
 A:Residues: 1-260 <ARM>
 A:Cross-references: EMBL:X65453; NID:950351; PIDN:CAA46448.1; PID:950352
 C:Keywords: glycoprotein; transmembrane protein
 F:23-46/Domain: transmembrane #status predicted <TMM>
 F:47-260/Domain: extracellular #status predicted <EXT>
 F:239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.48; Score 157; DB 2; Length 260;
 Best Local Similarity 24.88; Pred. No. 1.3e-05;
 Matches 75; Conservative 51; Mismatches 105; Indels 72; Gaps 16;

QY 32 PAPSAPAPAPPAASRSMFLALLIGL-GOVGCSIALFLYFRAQMDPNRISEDSHCFYR 90
 Db 8 PSRSVATGLP--ASMKIFMVLITVFLITQMGSAFVLYLHRLD--RVEEE----- 56
 QY 91 ILRLHE-----NAGLDQSTLESDTLPDSCRMKQAFQAGVQ-----KELQHV 134
 Db 57 -VNLHEDFVFIKLKRCNKGGSLSL-----NCEMRQFEDLVKDTLNKE----- 103
 QY 135 GPORFGAPAMGSLDVAORKEPAQFAHLTINAAISPSGSHKVTLSWYHGRWAK 194
 Db 104 -----EKENSF--EMRGDEDPQIAAHVYVSEA-----NSNAASVLQWAKKGYT 147
 QY 195 ISNMT-LSNGK-LRVNODGFYLYANICF-RHETSGSVPTDYQLQVMVYVVKTSIK--IP 249
 Db 148 KSNLVMLENGKQLTVRREGLYIYVTVTFCSNREPSSQRP-----FIVGLWLFPSIG 199
 QY 250 SSNLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVNSPSLLDPDQDATYFGA 309
 Db 200 SERILLKAANTHSSQLCEQQ--SVHLGGVFELOPGASVFVNVTASQVTHRVGFSFGL 257
 QY 310 FKV 312
 Db 258 LKL 260

RESULT 7

JQ1344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: JQ1344
 R: Su, X.; Morris, D.D.; McGraw, R.A.
 Gene 107, 319-321, 1991
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necr
 A:Reference number: JQ1344; MUID:92084125; PMID:1748301

C/Species: *Capra sp. (baboon)*
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

RESULT 12

QWJUN

tumor necrosis factor alpha precursor [validated] - human
 N:Alternate names: cachectin; TNFA
 C:Species: Homo sapiens (man)
 C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
 C:Accession: A93585; S6153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
 R:Medwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
 Nucleic Acids Res. 13, 6361-6373, 1985
 A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
 A:Reference number: A93585; MUID:86016093; PMID:2995927
 A:Accession: A93585
 A:Molecule type: DNA
 A:Residues: 1-233 <NED>
 A:Cross-references: GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 R:Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurke
 Nature Genet. 3, 137-145, 1993
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
 A:Reference number: S36152; MUID:93272029; PMID:8499947
 A:Accession: S36153
 A:Status: nucleic acid sequence not shown; translation not shown
 Molecule type: DNA
 Residues: 1-233 <IRI>
 A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
 Nature 312, 724-729, 1984
 A:Title: Human tumour necrosis factor: precursor structure, expression and homology to l
 A:Reference number: A93351; MUID:85086244; PMID:6392892
 A:Accession: A93351
 A:Molecule type: mRNA
 A:Residues: 1-233 <PEN>
 A:Cross-references: GB:X02910; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc
 R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.;
 Science 228, 149-154, 1985
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A:Reference number: A44189; MUID:85142190; PMID:3856324
 A:Accession: A44189
 A:Molecule type: mRNA
 A:Residues: 1-62, 5', 64-233 <WAN>
 A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
 R:Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
 Lymphokine Res. 7, 175-185, 1988
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
 A:Reference number: A61478; MUID:86301617; PMID:2841543
 A:Accession: B61478
 A:Molecule type: protein
 A:Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
 R:Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
 R. J. Biochem. 152, 515-522, 1985
 A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
 A:Reference number: I53311; MUID:86030296; PMID:3932069
 A:Accession: I53311
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-233 <NAR>
 A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
 A:Experimental source: U-937 cells
 R:Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A:Title: O-glycosylated species of natural human tumor-necrosis factor-alpha.
 A:Reference number: S62610; MUID:96202967; PMID:8631363
 A:Accession: S62610
 A:Molecule type: protein
 A:Residues: 77-99 <TAK>
 R:D'Alfonso, S.; Richiardi, P.M.
 Immunogenetics 39, 150-154, 1994
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter regio
 A:Reference number: I54522; MUID:94102809; PMID:7903959
 A:Accession: I54522
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-8 <DAL>
 A:Cross-references: GB:S68530; NID:g544751
 R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
 J. Exp. Med. 176, 1053-1062, 1992
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific
 A:Reference number: A59163; MUID:93018820; PMID:1402651
 A:Contents: annotation; identification of myristylated lysines
 R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Morfat, B.; Spencer, S.A.; Henzel, W.J.;
 J. Biol. Chem. 260, 2345-2354, 1985
 A:Title: Human tumor necrosis factor. Production, purification, and characterization
 A:Reference number: A92511; MUID:85130974; PMID:3871770
 A:Contents: annotation; disulfide bond
 C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after indu
 out detriment to normal cells. It can also act synergistically with interferon gamma
 C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes cl
 ut are produced by different cell types and have different induction kinetics.
 C:Genetics:
 A:Gene: GDB:TNF; TNFA
 A:Cross-references: GDB:120441; OMIM:191160
 A:Map position: 6p21.3-6p21.3
 A:Introns: 62/3; 78/1; 94/1
 C:Complex: homotrimer
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine;
 F:1-76/Domain: propeptide #status predicted <PRO>
 F:17-233/Product: tumor necrosis factor #status experimental <NAT>
 F:19-20/Binding site: myristate (Lys) (covalent) #status experimental
 F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
 F:145-177/Disulfide bonds: #status experimental
 Query Match 8.3%; Score 139.5; DB 1; Length 233;
 Best Local Similarity 24.9%; Pred. No. 0.00032;
 Matches: 48; Conservative 34; Mismatches 76; Indels 35; Gaps 9;
 QY 133 IVGPOREFGAPAMWEGSLDVAORGR---PEAQPFAHLTINAASIPSGSHKVTLSWYHD 189
 DB 55 VIGPOREFPRDLISLPLAQAVRSRRTPSPKPAHVAVN----PQAGQL---QWLNR 107
 QY 190 RGWAKISN-MTLNGLKRLVNDGFTYLYANICFRHETSGSVPTDYQL-----WVY 240
 DB 108 RANALLANGVELRDNLVVPSEGLYLYSQVLK----GGCPSHTVLLTHTISRIASVY 163
 QY 241 VVK---TSIKIPSSHNLMKGSTKNWNSSEHFYSINVGGFFKLRAEEISIQVNSPS 296
 DB 164 QTKVLLLSAIPKPCQRETPGEAEKFW-----YEPIYLGVPQLEKGRLSAEINRPD 216
 QY 297 LLD-PDQDATYFG 308
 DB 217 YLDFAESGGQVYFG 229
 RESULT 13
 A25451
 tumor necrosis factor alpha precursor - rabbit
 N:Alternate names: cachectin; TNF alpha
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: A25454; A25451; JS0727
 R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayash
 DNA 5, 149-156, 1986
 A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding fo
 A:Reference number: A25454; MUID:86219711; PMID:3519137
 A:Accession: A25454
 A:Molecule type: mRNA
 A:Residues: 1-234 <ITO>
 A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
 R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace,
 DNA 5, 157-165, 1986
 A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A:Reference number: A25451; MUID:86219712; PMID:3519138
 A:Accession: A25451
 A:Molecule type: DNA
 A:Residues: 1-234 <ITO>

A>Note: this sequence differs from that shown in having a Gln inserted between residues R;Shatkov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990

A>Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- α and TNF- β
A:Reference number: JH0309; MUID:91065534; PMID:2249779

A:Accession: J50727

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-62, 'Q', 63-234 <SHA>

A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756

C:Genetics:

A:Introns: 62/3; 80/1; 96/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane

F:1-81/Domain: propeptide status predicted <PRO>

F:82-234/Product: tumor necrosis factor status predicted <MAT>

F:19,20/Binding site: myristate (Lys) (covalent) status predicted

F:83/Binding site: carbohydrate (Ser) (covalent) status predicted

F:147-178/Disulfide bonds: status predicted

Query Match 8.2%; Score 137.5; DB 1; Length 234;

Best Local Similarity 22.6%; Pred. No. 0.00048;

Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

Qy 27 EGPLHPAPAPAPAPPPAASR-----SMELALIGLIGLVVCSIALFLYFRAQMDPNKRIS 81

Db 14 EGPL-----PKRAGGQGRKCLCLFSLFVAGATTFC-----LLHFRVIGPQEEES 63

Qy 82 EDSTHCFYRILRLHENAGLDSTLESDTLPSDCRRMKQAFQGAQVOKELQIHVIGPQFSG 141

Db 64 PNNLHLV-----NPVQAVMTLRS-----ASRALSDRPLAHVV----- 95

Qy 142 APAMGSLDVAORGPAPAPFAHLLINAAIPSGSHKVTLSWYHGRGWAKISN-MTL 200

Db 96 ANPQVEGQ-----LQWLSQRANALLANGMKL 121

Qy 201 SNGKLRYNODGYLYLANICPRHETSGVPTDYLQLMVYVKTSLKIPSSHNLKMG--- 257

Db 122 TDNLVVPADGLYLYSOVLF-----SGQGRSVTLTHVSRFVAVSPKVNLLSAKS 176

Qy 258 -----GSTRKNSGSEPHFYSINVGFFKLAGEEISIQVSNPFLD-PQDATYF 307

Db 177 PCHRETPAEAPMAW-----YEPYILGGVGFQLEKGRDLSTEVNQPEYLDLAESGGQVYF 229

Qy 308 G 308

Db 230 G 230

RESULT 14

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000

C:Accession: I54490

R:Crew, M.D.; Filipovsky, M.E.

Immunogenetics 35, 351-353, 1992

A>Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus

A:Reference number: I54490; MUID:92218012; PMID:1348497

A:Accession: I54490

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: TNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) status predicted

Query Match

8.1%; Score 135.5; DB 2; Length 235;

Best Local Similarity 25.1%; Pred. No. 0.0007;

Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

Qy 133 IVGPQRSGAP-----AMGEGSLDVAORGPAPFAHLLINAAIPSGSHKVTLSWY 185

Db 55 VIGPQREKFPNNLPITIGSMAQTILTRSSQSSD-KPVAHVAN-----HGVDBQL 105

Qy 186 WYHGRGWAKISNMTLSNG-KLRVNO-----DGFYLYLANICFRHETSGVPTDYLQLMV 239

Db 106 EWLRSRG-----ANALLANGMDLKDNLVLPADGLYLYVSOVLFKGGCCSYV-----LLT 155

Qy 240 YVVK-----TSIKIPSHNLKMGSTKNSGSEPHFYSINVGFFKLAGEEISIQ 286

Db 156 HTVSREAVSYEDKVNLLSAIKSPCKETPEGSELKPW-----YEPYILGGVGFQLEKGD 208

Qy 287 EISQVSNPFLD-PQDATYF 308

Db 209 RLSEAVNLPKRYLDFAESGQVYF 231

RESULT 15

I24642

tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: I46047; S24642

R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A>Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin

A:Reference number: I46046; MUID:94083525; PMID:8260599

A:Accession: I46047

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-233 <CL2>

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C:Genetics:

A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:20/Binding site: myristate (Lys) (covalent) status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) status predicted

F:145-177/Disulfide bonds: status predicted

Query Match 8.0%; Score 133.5; DB 1; Length 233;

Best Local Similarity 25.8%; Pred. No. 0.001;

Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

Qy 133 IVGPQR--FSGAPAMGEGSLDVAORGPAPFAHLLINAAIPSGSHKVTLSWY 187

Db 55 VIGPQRESPGPGSI--NSPLVQTLRSSQSSNKPVAHVAD-----INSPG 100

Qy 188 HDRGWAKISNMTLSNG-KLRVNO-----DGFYLYLANICFRHH-----ETSGSV 231

Db 101 QLRWDSYANALMANGVKLEDNLVVPADGLYLYVSOVLFKGGCCPSTPLFTHTRIA 160

Qy 232 TDYLQLMVYVKTSLKIPSSHNLKMGSTKNSGSEPHFYSINVGFFKLAGEEISIQ 291

Db 161 VSY-QTRVNL-SAIKSPCHRETPPEWAEAKPW-----YEPYILGGVGFQLEKGRDLSAE 211

Qy 292 VSNPFLD-PQDATYF 308

Db 212 INLPDYLYAESGQVYF 229

Search completed: April 16, 2003, 12:20:42

Job time : 17.5 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:16:16 ; Search time 9.5 seconds
(without alignments)
1379.634 Million cell updates/sec

Title: US-09-787-126-4

Perfect score: 1675

Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPDQDARYFGAKVQDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	1	TN11_MOUSE
2	1597	95.3	318	1	TN11_MOUSE
3	1417.5	84.6	317	1	TN11_HUMAN
4	258.5	15.4	281	1	TN10_HUMAN
5	244	14.6	291	1	TN10_MOUSE
6	188.5	11.3	261	1	TN10_MOUSE
7	185.5	11.1	261	1	TN10_MOUSE
8	183	10.9	278	1	TN10_MOUSE
9	182.5	10.9	261	1	TN10_MOUSE
10	182	10.9	279	1	TN10_MOUSE
11	179.5	10.7	282	1	TN10_MOUSE
12	178	10.6	280	1	TN10_MOUSE
13	177	10.6	280	1	TN10_MOUSE
14	176.5	10.5	261	1	TN10_MOUSE
15	173.5	10.4	281	1	TN10_MOUSE
16	171.5	10.2	261	1	TN10_MOUSE
17	168.5	10.1	272	1	TN10_MOUSE
18	164	9.8	260	1	TN10_MOUSE
19	159.5	9.5	261	1	TN10_MOUSE
20	157	9.4	234	1	TN10_MOUSE
21	157	9.4	260	1	TN10_MOUSE
22	154	9.2	260	1	TN10_MOUSE
23	151	9.0	240	1	TN10_MOUSE
24	149	8.9	234	1	TN10_MOUSE
25	148.5	8.9	233	1	TN10_MOUSE
26	147.5	8.8	233	1	TN10_MOUSE
27	147.5	8.8	310	1	TN10_MOUSE
28	146.5	8.7	235	1	TN10_MOUSE
29	146.5	8.7	239	1	TN10_MOUSE
30	145	8.7	260	1	TN10_MOUSE
31	143.5	8.6	233	1	TN10_MOUSE
32	143.5	8.6	233	1	TN10_MOUSE
33	141	8.4	234	1	TN10_MOUSE

34	140	8.4	174	1	TN15_HUMAN
35	140	8.4	233	1	TNFA_FELCA
36	139.5	8.3	233	1	TNFA_CANFA
37	139.5	8.3	233	1	TNFA_HUMAN
38	139	8.3	234	1	TNFA_CAPHI
39	137	8.2	235	1	TNFA_RABIT
40	135.5	8.1	235	1	TNFA_PERLE
41	134.5	8.0	240	1	TN14_HUMAN
42	133.5	8.0	233	1	TNFA_BOVIN
43	133	7.9	232	1	TNFA_PIG
44	129.5	7.7	233	1	TNFA_MARMO
45	129.5	7.7	235	1	TNFA_RAT

ALIGNMENTS

RESULT 1

ID	TN11_MOUSE	↑ STANDARD;	PRT;	316 AA.
AC	O35235; O35306; O9R1V0; O9JJK8; Q9JJK9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor) (OCIF).			
GN	TNFRSF11 OR RANKL OR TRANCE OR OPGL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Hybridoma;			
RX	MEDLINE=37460112; PubMed=9312132;			
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;			
RT	"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";			
RL	J. Biol. Chem. 272:25190-25194(1997).			
RN	[2]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Thymic lymphoma;			
RX	MEDLINE=98032977; PubMed=9367155;			
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;			
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";			
RL	Nature 390:175-179(1997).			
RN	[3]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=9827661; PubMed=9568710;			
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;			
RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";			
RL	Cell 93:165-176(1998).			
RN	[4]			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Bone marrow stroma;			
RX	MEDLINE=9818248; PubMed=9520411;			
RA	Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M., Mochizuki S.-I., Tomoyasu A., Yan K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;			

DR	EMBL; AF013171;	AC53762.1;	-
DR	EMBL; AB037599;	BAA90488.1;	-
DR	HSP; P50591;	IDOG.	-
DR	GeneW; HGNC:11926;	TNFSF11.	-
DR	MIM; 602642;	-	-
DR	InterPro; IPR003636;	TNF_abc.	-
DR	InterPro; IPR000478;	TNF_family.	-
DR	Ffam; PF00229;	TNF; 1.	-
DR	PRODOM; PD002012;	TNF_abc; 1.	-
DR	SMART; SM00207;	TNF; 1.	-
DR	PROSITE; PS00251;	TNF_1;	FALSE_NEG.
DR	PROSITE; PS50049;	TNF_2;	1.
KW	Cytokine; Differentiation;	Receptor; Glycoprotein;	Transmembrane;
KW	Signal-anchor;	Alternative splicing.	-
FT	CHAIN	1	317
FT	CHAIN	140	317
FT	DOMAIN	1	47
FT	TRANSMEM	48	68
FT	DOMAIN	69	317
FT	SITE	139	140
FT	CARBOHYD	171	171
FT	CARBOHYD	198	198
FT	VARSPLIC	1	47
FT	VARSPLIC	1	73
FT	CONFLICT	194	194
FT	SEQUENCE	317 AA;	35478 MW; 766176446348097f CRC64;
Qy	Query Match	84.6%;	Score 1417.5; DB 1; Length 317;
Qy	Best Local Similarity	84.3%;	Pred. No. 5e-110;
Qy	Matches 268;	Conservative 16;	Mismatches 31; Indels 3; Gaps
Qy	1 MRRASRDYGYKLRSSEMGSGPGVNEGPHAPSA	PAPAPPAA	SRSMFLALLGLGLGQ 60
Dd	1 MRRASRDYTYLKGSEMGSGPGAPHEGPLH	APPPPAQP	PPAASRMFMVALLGLGLGQ 59
Qy	61 VVCSTALFLYFRQMDDNRISTESTHCFFYLRLKLNAGLOSTLESDT	--LPQSCRM 118	
Dd	60 VCVSVALFFFRQMDDNRISEDGTCHLYRLKLNHNADFDTLLSQDKLIPOSCRRI	119	
Qy	119 KQAFQGAQVKELQHIVGPBFSGAPAMGESWLVDVAQRGKPEAQPPAHITINNAISIPGS	178	
Dd	120 KQAFQGAQVKELQHIVGSHIRAEKAMVDGSLDLAKRSLKEAQAQPPAHITINATDIPGS	179	
Qy	179 HKVTLSWYHDGRGWAKISNTLTNGKLRYNODGFYYLYANICFRHHETSSGVPDYQLQM	238	
Dd	180 HKVSLSSWYHDGRGWAKISNTLTNGKLRYNODGFYYLYANICFRHHETSGDATEYQLQM	239	
Qy	239 YVVYKTSIKIPSSHLMKGGSTKNWSGNSEFHYSINVGGFKPLRAGEBISIQVNSPLL	298	
Dd	240 YVVYKTSIKIPSSHLMKGGSTKYWSGNSEFHYSINVGGFKPLRSGEIEISVNSPLL	299	
Qy	299 DPQQDATYFGAFKVQDID 316		
Dd	300 DPQQDATYFGAFKVRIID 317		
RESULT 4			
TD10_HUMAN	TD10_HUMAN	STANDARD;	PRT; 281 AA.
AC	P50591;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related		
DE	apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).		
GN	TNFSF10 OR TRAIL OR APO2L		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI	TXID:9606;		

[1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 RL family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-96278649; PubMed-8663110;
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
 RA Askenazi A.;
 RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
 RL necrosis factor cytokine family.";
 RL J. Biol. Chem. 271:12687-12690(1996).
 [3]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE-20017054; PubMed-10549288;
 RA Hynowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Askenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RL complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed-10542098;
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RL specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 [5]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE-99413670; PubMed-10485660;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.-C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 RL selective antitumor activity.";
 RL Immunity 11:253-261(1999).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 CC AND PROSTATE.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL; U37518; AAC50332.1; -
 DR EMBL; U57059; AAB01233.1; -
 DR Genbank; HGNC:11925; TNFSF10.
 DR MIM; 603598; -
 DR PDB; 1D0G; 22-OCT-99.
 DR PDB; 1D4V; 01-NOV-99.
 DR PDB; 1D2Q; 11-FEB-00.
 DR InterPro; IPR003636; TNF abc.
 DR InterPro; IPR000478; TNF_family.

DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 KW Zinc; 3D-structure.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT DOMAIN 39 281 (POTENTIAL).
 FT METAL 230 230 EXTRACELLULAR (POTENTIAL).
 SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAB2F6D CRC64;
 ZINC.
 Query Match 15.48; Score 258.5; DB.1; Length 281;
 Best Local Similarity 26.48; Pred. No. 3e-14;
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
 QY 43 PAASRSMFLALLGLGIGVGVCSIALFLYFRAQMD--PNRISEDSHCFYRILRLHENAGL 100
 DB 10 PSLGTCVLIIVFVLQSLCVAVTYVYFTELKQMDQKYSKGIACF-----LKEDDSY 64
 QY 101 QDSTLESDTLPDSCRRMKQAFQGAQVK-----ELQHVGPQRFSGAPAM 146
 DB 65 WDP--NDEESMNSPCWQVQWOLRLVRKMLRTSEETISTVQEKQNISPL----- 113
 QY 147 EGSWLDVAQRGPEAQPEAHLT-----INAAISPGSHKVTL-----SSWYHDR-GWAKIS 196
 DB 114 -----VREGRPQVRA--AHITGTRSRNTLSSPSKNEKALGRKINSWESSRSGHSFLS 165
 QY 197 NMTLSNGRLRVNODGFIYLANICPRHETSGVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
 DB 166 NLHLANGELVHERGFIYISOTYFRFQEEKENTKNDKQWQYIYKYT-SPDPILLMK 224
 QY 257 GGSTRKNSGSEFHFYSINVGGFKLRAEEISIOVSNPSLLDPODQATYFGAFKY 312
 DB 225 SARNCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280
 RESULT 5
 TN10_MOUSE
 ID TN10_MOUSE STANDARD; PRT: 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 RL family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC -----
 DR EMBL: U37522; AAC52345.1;
 DR HSP: P50591; 1D0G.
 DR MGD: MG1:107414; Tnfsl10.
 DR InterPro: IPR003636; TNE_abc.
 DR Pfam: PF00229; TNE; 1.
 DR ProDom: PD002012; TNE; 1.
 DR SMART: SM00207; TNE; 1.
 DR PROSITE: PS00251; TNE_1; 1.
 DR PROSITE: PS50049; TNE_2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
 CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
 SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;

Query Match 14.6%; Score 244; DB 1; Length 291;
 Best Local Similarity 27.5%; Pred. No. 4.9e-13;
 Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

QY 52 ALLIGLIGLQ-----VVCSTAL-----FLYRAQMD--PNRISESTHCFYRIL 92
 DB 6 ALKDLFSQHFRRMVICVILVLLQAVSVAVTYFTNEMKQLDNYSKIGLACFSK-- 63
 QY 93 RLHENAGLQDSTLESDTLPSDC-----RRMKAQAFQAVQKELQHVIG--PQFSGAPAMM 146
 DB 64 ----TDEDFWDT--DGEILNRPCQVKRQLYQIEVTLRTFDITVPEKQLSTPPPLP 118
 QY 147 EGSWLDVAQGRPEAOPFAHLT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS 196
 DB 119 RG-----GRPQ-KVAAHITGTRNSALIPISKDKGTGLQKIESSESRKGHSLN 169
 QY 197 NMTLSGKLAVNQDGYLYANICFRHHE---TSGSVPTDYL---QIMVYVKTISKIPS 250
 DB 170 HVLFRNGELVIEQGLYIYSQTYFRFOEAEDASRMVSKDKVTKQLQVQIYKYIT-SYDP 228
 QY 251 SHNLMGSGTKNWSSEHFYSINVGFFKLRAGEISIOVSNPDLDPDQDQATYFGAF 310
 DB 229 PIVLMSARNWSRDRYGLKSIYOGGLFELAKNDRIFFSVTNEHMLDLDQASFFGAF 288
 311 KV 312
 DB 289 LI 290

RESULT 6
 TNF5_CALJA STANDARD; PRT; 261 AA.
 ID TNF5_CALJA
 AC Q9BDN3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
 DE L) (CD154 protein).
 GN TNFSF5 OR CD40LG OR CD40L.
 OS Callitrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
 OC Callitrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;

RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 FT "Cloning, sequencing, and homology analysis of nonhuman primate
 FT Fas/Fas-ligand and co-stimulatory molecules";
 RL Immunogenetics 53:315-328(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
 CC proliferation in the absence of co-stimulus as well as TGE
 CC production in the presence of IL-4. Involved in immunoglobulin
 CC class switching (By similarity).
 CC -!- SUBUNIT: HOMOTRIMER (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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DR EMBL: AF344844; AAK37603.1;
 DR HSP: P29965; ITALY.
 DR InterPro: IPR003263; TNE 5.
 DR InterPro: IPR003636; TNE_abc.
 DR InterPro: IPR000478; TNE_family.
 DR Pfam: PF00229; TNE; 1.
 DR ProDom: PD002012; TNE_abc; 1.
 DR ProDom: PD008600; TNE 5; 1.
 DR SMART: SM00207; TNE 1;
 DR PROSITE: PS00251; TNE_1; 1.
 DR PROSITE: PS50049; TNE_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 MEMBER 5, MEMBRANE FORM.
 FT 113 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
 FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 23 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 44 261 EXTRACELLULAR (POTENTIAL).
 FT SITE 112 113 CLEAVAGE (BY SIMILARITY).
 FT DISULFID 178 218 POTENTIAL.
 FT CARBOHYD 240 240 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 261 AA; 29360 MW; 10CA588D923734EB CRC64;

Query Match 11.3%; Score 188.5; DB 1; Length 261;
 Best Local Similarity 25.8%; Pred. No. 1.7e-08;
 Matches 77; Conservative 49; Mismatches 110; Indels 63; Gaps 16;

QY 32 PAPSAPAPAPPAAASRMFLALIGLIGLQGVCSIALF-LYFRAQMDPNRISESTHCFYR 90
 DB 8 PVPRSAATGPP--VSMKIPMYLLTVFLITQMGISALFAVYLHRRLD--KIEDER----- 57
 QY 91 ILRLHE-----NAGLQDSTLESDTLPSDCRRMKAQAFQAVQKELQHVIGPQRF 139
 DB 58 ---NLHEDFVFMKTIOCNTEGERSLSL-----NCEIKSQEGFV-KDIM-----L 100
 QY 140 SGAPAMGSEWLDVAQGRPEAOPFAHLTINAAISPSGSHKVTLSWYHDRGWAKIS-- 137
 DB 101 NKEEKKNSF--EMQKQDNQPIAAHV-----ISEASKTSLVLOAEKGYTMSNNL 152
 QY 198 MTLNKGK-LRVNQDGYLYANICF-RHETSGSVPTDYLQLMVYVKTISKIPSHN-- 253
 DB 153 VTLENGKQLTVKROGLYIYAQVTFCSNREASSQAP-----FIASLCLKPPNRFERI 204
 QY 254 LMKGSGTKNWSSEHFYSINVGFFKLRAGEISIOVSNPDLDPDQDQATYFGAFV 312
 DB 205 LLRAANTH--SSAKPGQOSIHLGGILFQLOPGASVFNVTDFPSQVSHGFTGFTSGLLKL 261

RESULT 7
TNF5_BOVIN STANDARD; PRT; 261 AA.
ID TNF5_BOVIN AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
DE tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
GN TNF5 OR CD40L OR CD40L.
OS Bos taurus (Bovine)
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
P. TISSUE=Blood;
RX MEDLINE=96006582; PubMed=7590981;
RA Mertens B.E.L.C.; Muriuki M.; Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RT and tumor necrosis factor alpha.";
RL Immunogenetics 42:430-431(1995).
CC -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z48469; CAA8363.1; --
CC HSP; P29965; ITALY.
CC InterPro: IPR003263; TNF_5.
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD008600; TNF_5; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS00049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC CHAIN 1 261
FT CHAIN 113 261
FT CHAIN 113 261
FT DOMAIN 1 22
FT TRANSMEM 23 46
FT DOMAIN 47 261
FT SITE 112 113
FT DISULFID 178 218
FT CARBOHYD 240 240
FT SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787DF CRC64;
Query Match. 11.18; Score 185.5; DB 1; Length 261;
Best local Similarity 25.18; Pred. No. 3e-08;
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;
QY 32 PAPSAPAPPAPASRSMFALLGLGQVVCSTALF-LYFRAQMDPNRISDSTHCYFR 90

Db 8 PPSRSVATGPP--VSNKIFMYLLTVLITOMIGSALFAVYLHRRLO--KIEDER----- 57
QY 91 ILRLHE-----NAGLDQSTLESEDTLPDSCEMKQAQOGAVQKELQHVGPORF 139
Db 58 --NLHEDVFEMKTICRNKGEGLSL-----NCEEIRSFEDLVKIDMGN-----KEY 104
QY 140 SGAPAMMEGSLDVAORGKPEAOPFAHLTINAAISIPSGSHKVTLSHWHDRGWAISN-- 197
Db 105 KKEKKEFE-----MHKGDQEPQIAHV-----ISEASSKTSVLQWAPKGYITLSNNL 152
QY 198 MTLNKGK-LRVNQDGFYLLYANICF-RHETSGVPTDYQLQVMYVVKTSIKIPSSN-- 253
Db 153 VTLENGQLAKVKGQFYIYVQVTFCSNRETLSQAP-----FIASLCLKSPSGSERI 204
QY 254 LMKGGSTKNSGSEPHFYINVGPFKLRAGEISIOVNSPISLLDPDQDQATYGAQKV 312
Db 205 LLRAANTH--SSSKPCGQOQSIHLGGVELOSASVFNVTDPQVSHGTFSTGLLKL 261
RESULT 8
TNF6_RAT STANDARD; PRT; 278 AA.
ID TNF6_RAT AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
GN TNFRSF6 OR FASL OR APTLGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94084792; PubMed=7505205;
RA Suda T.; Takahashi T.; Golstein P.; Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family.";
RL Cell 75:1169-1178(1993).
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects (By similarity).
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC
CC EMBL; U03470; AAC52129.1; --
CC HSP; P01375; 4TSV.
CC InterPro: IPR003636; TNF_abc.
CC InterPro: IPR000478; TNF_family.
CC Pfam; PF00229; TNF; 1.
CC ProDom; PD002012; TNF_abc; 1.

-I- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

-I- SUBUNIT: HOMOTRIMER (By similarity).

-I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

-I- FM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

-I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; AF344860; AAK37542.1; HSP; P29965; ITALY.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_ab.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_ab; 1.
ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50045; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 261
FT CHAIN 113 261
FT DOMAIN 1 22
FT TRANSMEM 23 43
FT DOMAIN 44 261
FT SITE 112 113
FT DISULFID 178 218
FT CARBOHYD 240 240
SQ SEQUENCE 261 AA; 29357 MW; 85E1388B507901B5 CRC64;

Query Match 10.9%; Score 182.5; DB 1; Length 261;
Best Local Similarity 25.8%; Pred. No. 5.2e-08;
Matches 77; Conservative 49; Mismatches 110; Indels 63; Gaps 16;

Qy 32 PAPSAAPAPPASRSFMFLALLGLIGQQVVCSTALF-LYFRAQMDPNRIESTHCFYR 90
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 8 PAPRSAATGLP-VSMKIFMTLLVFLLITOMIGSALFAVYLHRRLD-KIEDER----- 57
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 91 ILRLHE-----NAGLDSTLESEDTLPSDCRMKQAFQAVOKELQHIVGPQR 139
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 58 --NLHEDVFVKTTORCHTNGERSLL-----NCEIKSQEGFV-KDTM-----L 100
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 140 SCAPAMGSLWDLVAQKPKPAQPFAHLTINAAISPGRSHKVLTSSWYHDRGWAKIS-- 197
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 101 NKEKKENSF-EMKGKDNPQIAAHV-----ISEASKTSTVLQAEKGYTMSNNL 152
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 198 MTLNGK-LRVNDGFYYLIYANICF-RHHETSGSVPTDYLOLMVVVKTSTIKIPSSH-- 253
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 153 VTLENGKLTVKRGLYIIYAQVTFCNSREASQAP-----FIASCLCKPPNRPERI 204
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Qy 254 LMKGSYKNWGNSEFFHYISNVGGFFKLAGEELISIOVSNPLSDPDQDATYCAFKV 312
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db 205 LLRAANTH--SSAKPCGOOSTHLGGIFELOPGCASVFNVTDPQSQVHGCTGFTSFGLKL 261
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 10
TNF6_MOUSE STANDARD; PRT; 279 AA.
AC P41047; Q9R1F2;

RESULT 12
 TNF6_MACNU STANDARD; PRT; 280 AA.
 AC Q9M16; Q9BDM5;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (CD95L protein)
 GN TNFSF6 OR FASL OR CD95L.
 OS Macaca mulatta (Rhesus macaque);
 OS Macaca fascicularis (Crab eating macaque);
 OS Macaca nemestrina (Pig-tailed macaque);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544, 9541, 9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 RA Kiril Y., Inoue T., Yoshino K.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
 transduces the apoptotic signal into cells. May be involved in
 cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
 peripheral tolerance, in the antigen-stimulated suicide of mature
 T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
 modulates its effects (By similarity).
 CC -1- SUBUNIT: Homotrimer (Potential).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF344856; AA037539.1;
 CC EMBL; AB035138; BAA90294.1;
 CC EMBL; AB035139; BAA90295.1;
 CC EMBL; AB035140; BAA90296.1;
 CC HSPF; P01375; 4TSV.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR000478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNFCROSISFCT.
 DR PRODOM; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT CHAIN 129 280 MEMBER 6, MEMBRANE FORM.
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
 FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT DOMAIN 102 280 (POTENTIAL).
 FT DOMAIN 4 69 EXTRACELLULAR (POTENTIAL).
 FT SITE 128 129 POLY-PRO.
 FT SITE 201 232 CLEAVAGE (BY SIMILARITY).
 FT CARBOHYD 183 183 POTENTIAL.
 FT CARBOHYD 249 249 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAc...) (POTENTIAL).
 FT CONFLICT 60 60 S -> P (IN REF. 1).
 SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
 Query Match 10.6%; Score 178; DB 1; Length 280;
 Best Local Similarity 22.0%; Pred. NO 1.4e-07;
 Matches 68; Conservative 44; Mismatches 105; Indels 92; Gaps 10;
 QY 22 PGVHEGPHAPAPAP--APPAAARS-----MFLALGLGLGVVCS 65
 DB 46 PPPPPPPPPPPPPPPPLPLPLPKKRNHSTGLLLVMFMVLAVALVGLGLG----- 99
 QY 66 ALFLYFRQMDPNRISDSHCFYRLRLHFNAGLQDSTLESDTLPDSCRRMKQAFQGA 125
 DB 100 -MFQLFHLQ-----KELALRETSQRHTA-----SS 125
 QY 126 VKELOHIVGPQRFSGAPAMBSGMDVAQRCKPAQPAHLT--INAAIPSGSHKVTL 183
 DB 126 LEKQIGHSPPE-----KKQKVAHLTGKPNKSNP----- 158
 QY 184 SSWHGRGWAKISNNMTLSNGLRVNODGFYLLYANICFRHETSGSVPTDYQLQAVYVK 243
 DB 159 LEWEDTYGIVLLSGVKKKGLVINETGLYFVYSKYFRGQCTN-----LPLSHKVM 212
 QY 244 TSIKIPSSHNLMKGGSTNNNSSEHFYSINVGFFKLAGEEISIQVSNPILDPDQD 303
 DB 213 RNSKYPODLVME--GRMSYCTTGQMAHSSYLGAVNLTADHLVYVNSLSLVNFEES 271
 QY 304 ATYFGAFKV 312
 DB 272 QTFFGLYKL 280
 RESULT 13
 TNF6_CERTO STANDARD; PRT; 280 AA.
 AC Q9BDM1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (CD95L protein)
 GN TNFSF6 OR FASL OR CD95L.
 OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercocebus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
 transduces the apoptotic signal into cells. May be involved in
 cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
 peripheral tolerance, in the antigen-stimulated suicide of mature
 T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
 modulates its effects (By similarity).
 CC -1- SUBUNIT: Homotrimer (Probable).

SEQUENCE FROM N.A.
Wilkinson J.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

[7]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-Blood;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

[8]
SEQUENCE OF 1-10 FROM N.A.
TISSUE-Blood;
Matsumura M., Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

[9]
CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
Tersikh A., Peitsch M.C., Tschopp J.;
Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
J. Biol. Chem. 272:18827-18833(1997).

[10]
PROCESSING.
PubMed-9427603;
Tanaka M., Itai T., Adachi M., Nagata S.;
Downregulation of Fas ligand by shedding.";

[11]
FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects.

[12]
SUBUNIT: HOMOTRIMER (PROBABLE).

[13]
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL SURFACE.

[14]
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2;
are produced by alternative splicing.

[15]
PTM: N-glycosylated.

[16]
PTM: The soluble form derives from the membrane form by proteolytic processing.

[17]
DISEASE: Defects in TNFSF6 are a cause of autoimmune lymphoproliferative syndrome (ALPS), also known as Canale-Smith syndrome (CSS), a childhood syndrome involving hemolytic anemia and thrombocytopenia with massive lymphadenopathy and splenomegaly.

[18]
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

[19]
DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/3338769674.g.htm".

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EMBL; X89102; CAA61474.1; --
EMBL; U08137; AAC50071.1; --
EMBL; U11821; AAC50124.1; --
EMBL; D38122; BAA07320.1; --
EMBL; AF288573; AAG60017.1; --
EMBL; Z66050; CAB09424.1; --
EMBL; BC017502; AAH17502.1; --
EMBL; AB013303; BRA32542.1; --
HSP; P01375; ITNF
Gene; HGNC:11936; TNFSF6.
MIM; 134638; --
MIM; 601859; --
InterPro; IPR003636; TNF_abcd
InterPro; IPR000478; TNF_family.

Search completed: April 16, 2003, 12:18:59
Job time : 10.5 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	263.5	15.7	214	13 Q9DD25	Q9ddz5 brachydanio
2	217.5	13.0	287	13 Q9QWT9	Q9Qwt9 gallus gall
3	149	8.9	234	6 Q9TJ33	Q9Ttj3 equus caball
4	142	8.5	232	4 Q9U1V3	Q9Uiv3 homo sapien
5	133.5	8.0	215	11 Q99ND1	Q99nd1 tamiasciuru
6	133	7.9	157	4 Q43647	O43647 homo sapien
7	132	7.9	149	6 Q97543	Q97543 actus nancy
8	132	7.9	217	11 Q9ERG6	Q9erg6 peromyscus
9	131.5	7.9	156	11 Q912L4	Q91z14 sigmodon hi
10	131	7.8	149	6 Q97538	Q97538 actus vocif
11	131	7.8	149	6 Q9TGG8	Q9Ttgg8 actus nlgrt
12	130	7.8	216	11 Q7O332	O7O332 mesocricetu
13	127.5	7.6	217	6 Q9BEC5	Q9Bec5 tenrec ecau
14	126.5	7.6	217	6 Q9BEG1	Q9Beg1 bradypus tr
15	126.5	7.6	217	6 Q9BEG0	Q9Beg0 cyclops da
16	126	7.5	216	6 Q9BEC9	Q9Bec9 ochotona pr

2 КЛАСТРАТИСКВ

117 RMKQAFQGA VOKELQHIVGPQRFSGAPAMME-----GS--WLDVAQRCKPEAQPFahlTI 169
QY
2 KLaEGIKaYISKVTDSIISKOTLHAARTOHSYNTGSKFNTVMOR-----PSaHlTL 55
db

GN	TNFA.
OS	Equus caballus (Horse).
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus...
OC	NCBI_TaxId-9796;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	STRAIN=THOROUGHRED; TISSUE=ARTERIAL ENDOTHELIUM;
RA	Ishida N., Sato F., Hasegawa T.;
RA	"Molecular cloning of equine tumor necrosis factor-alpha mRNA."
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

```

DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR ProDom: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00261; TNF 1; 1.
DR PROSITE: PS50049; TNF 2; 1.
DR _SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21E377 CRC64;

Query Match 8.9%; Score 149; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 4.1e-05;
Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps

QY 133 IVGPQPSGAPAMEGSWLDVAORK-----PRAQFPAHITINASIPSGSHKVTLSSTY 187
55 VIGPQREQLPNFAQ-SINPLAQTLRSSSTPDKPVAHVAN---PQAEGL---OWL 106

Db 188 HDRGWAQISN-WTLSNGKLVNODGFYLYANICFRRHETSGVDPYDQLQVMVVKTSI 246
107 SGRNALLANGVKLTQNLVPLDGLYLIYSQVLEK-----GQCPSTHVLTTTISRSLV 162

QY 247 KIPSHNLMKG-----GSTKNWNSGEFFHYISINVGGFPKLRAGEEISTOVSN 294
163 SYPSKVNLLSAIKSLANTESPEQAERKPW-----YEPYLLGVGFQPKGQDLSAEINQ 215

```

QY 295 PSLD-PQDQATYFG 308
 Db 216 PNYLFAESGQVYFG 230

RESULT	4
Q9UIV3	
ID	PRELIMINARY; PRT; 232 AA.
AC	Q9UIV3
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Tumor necrosis factor.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=93272029; PubMed=8499947;
RA	Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
RA	Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
RT	"dense Alu clustering and a potential new member of the NFkapab

SEQUENCE FROM N.A.
MEDLINE-96215741; PubMed-8629302;
Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
Wallace A.F., Russell M.E.;
"Allograft inflammatory factor-1. A cytokine-responsive macrophage
molecule expressed in transplanted human hearts.";
Transplantation 61:1387-1392(1996).

[3]
 RP MEDLINE-96006565; PubMed-7590964;
 RA Holzinger I., de Baey A., Messer G., Kick G., Zwierzina H.,
 RA Weiss E.H.;
 RT "Cloning and genomic characterization of LST1: a new gene in the human
 RT TNF region.";
 RL Immunogenetics 42:315-322(1995).
 [4]
 RP MEDLINE-9320881; PubMed-7916655;
 RA Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,
 RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
 RT "lymphotoxin-beta: A new member of the TNF family that forms a
 RT heteromeric complex with lymphotoxin on the cell surface.";
 RL Cell 72:847-856(1993).
 [5]
 RP MEDLINE-86016093; PubMed-2995927;
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D., Jarrett-Nedwin J.,
 RA Pennica D., Goeddel D.V., Gray P.W.;
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RT homology and chromosomal localization.";
 RL Nucleic Acids Res. 13:6361-6373(1985).
 [6]
 RP MEDLINE-91086846; PubMed-1670638;
 RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
 RA Riethmuller G., Weiss E.H.;
 RT "Polymorphic Structure of the Tumor Necrosis Factor (TNF) Locus: An
 RT Ncol Polymorphism in the First Intron of the Human TNF-beta Gene
 RT Correlates with A Variant Amino Acid in Position 26 and a Reduced
 RT Level of TNF-beta Production.";
 RL J. Exp. Med. 173:209-219(1991).
 [7]
 RP MEDLINE-91139175; PubMed-1671667;
 RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
 RT "Haplotypic polymorphisms of the TNFB gene.";
 RL Immunogenetics 33:50-53(1991).
 [8]
 RP MEDLINE-94362679; PubMed-8081366;
 RA Albertella M.R., Campbell D.R.;
 RT "Characterization of a novel gene in the human major
 RT histocompatibility complex that encodes a potential new member of the
 RT I kappa B family of proteins.";
 RL Hum. Mol. Genet. 3:793-799(1994).
 [9]
 RP MEDLINE-95324911; PubMed-7601445;
 RA Peelman L., Chardon P., Nunes M., Renard C., Geffrotin C., Valman M.,
 RA Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,
 RA Strominger J., Spies T.;
 RT "The BA1 Gene in the MHC Encodes an Evolutionarily Conserved Putative
 RT Nuclear RNA Helicase of the D-E-A-D Family.";
 RL Genomics 26:210-218(1995).
 [10]
 RP MEDLINE-20132445; PubMed-10668961;
 RA Neville M.J., Campbell R.D.;
 RT "Alternative splicing of the LSP-1 gene located in the major
 RT histocompatibility complex on human chromosome 6.";
 RL DNA Seq. 8:155-160(1997).
 [11]
 RP MEDLINE-98035883; PubMed-9367684;
 RA de Baey A., Fellerhoff B., Waier S., Martinuzzi S., Weidle U.,
 RA Weiss E.H.;
 RT "Complex expression pattern of the TNF region gene LST1 through
 RT differential regulation, initiation, and alternative splicing.";
 RL Genomics 45:591-600(1997).
 [12]

SEQUENCE FROM N.A.
 RP MEDLINE-98149985; PubMed-9480751;
 RA Shima T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
 RA Goto K., Mizuki N., Watanabe K., Fukuzumi Y., Taguchi S., Sugawara C.,
 RA Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
 RA Kimura M., Inoko H.;
 RT "Nucleotide sequencing analysis of the 146-kilobase segment around the
 RT IkbL and MICA genes at the centromeric end of the HLA class I
 RT region.";
 RL Genomics 47:372-382(1998).
 DR EMBL: Y14769; CAA75070.1; -
 DR HSP; P01375; 4TSV.
 DR InterPro: IPR003636; TNF_family.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PRODOM: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS00449; TNF_2; 1.
 SQ SEQUENCE 232 AA; 25446 MW; E4D71B19C6AE0D03 CRC64;
 Query Match 8.5%; Score 142; DB 4; Length 232;
 Best Local Similarity 24.5%; Pred. No. 0.00017;
 Matches 48; Conservative 37; Mismatches 69; Indels 42; Gaps 11;
 QY 133 IVGPQR--FSGAPAMEGSWLDVAQRGK-----PQAQFAHLTINAAIPSGSHKVTLSW 186
 DB 55 VIGPQREFPRDLSLIS-----PLAQAGSSRTSPDKVAHVAN-----PQAEGL---QW 103
 QY 187 YHGRGWAKISN-MTSLNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLQ----- 237
 DB 104 LRRANALLANGVELRDNLVWPSEGLYLYSQVLFK---GQCSTHVLITHTISRIA 159
 QY 238 MVYVVK-----TSIKIPSSHNLKGGSTKNGNSNFHYISVNGVFKLRAGEISIQVS 293
 DB 160 VSYQTKVNLISAIKSPCQRETPEGAERPW-----YEPYLGQVQLKGRDLSAEIN 212
 QY 294 NPSLLD-PDQATYFG 308
 DB 213 RPYLDFAESGQVYFG 228
 RESULT 5
 Q99ND1 ID Q99ND1 PRELIMINARY; PRT; 215 AA.
 AC Q99ND1
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor (Fragment).
 GN TNFA.
 OS Tamiasciurus hudsonicus (American red squirrel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Tamiasciurus
 OX NCBI_TaxID=10009;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA van Dijk M.A.M., de Jong W.W.;
 RT "Indels indicate that rodents are monophyletic and lagomorphs are
 RT their sister group.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ286824; CAC28540.1; -
 DR HSP; P06804; 2TNF.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR00478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR PRODOM: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS00449; TNF_2; 1.

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FT NON_TER 1 1
FT NON_TER 215 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match
Best Local Similarity 8.0%; Score 133.5; DB 11; Length 215;
Matches 45; Conservative 30; Mismatches 71; Indels 39; Gaps 7;

QY 133 IVGPQRF---SCAPAMGSLDVAQRGK-PEAQPFAHLTINAASIPSGSHKVTLSWYH 188
Db 46 VIGPQREPPNNPLPSAQAQMLTRSSQNMDKPAHVAVNQT-----EQQLWLS 97

QY 189 DRGWAKISN-MTSLNGKLRVNODGYIYANICFRHETSGSVPTDYQLMYVYVK----- 243
Db 98 RRANALLANGMELIDNQLWVPADGLYIYQVLFQGGCSTV-----LLTHTVSRFAV 151

QY 244 -----TSKIPSSHNLKGGSTKNWSEHFYSINVGFFKLKLRAGEEISIOVSN 294
Db 152 SYQDKVNLISAISPKESLEGAEPKW-----YEPYLGGVFQKGRDLSAEVNL 204

QY 295 PSLD 299
205 PSYLD 209

RESULT 6
ID 043647 PRELIMINARY; PRT; 157 AA.
AC 043647;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DE 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
CN TNFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF043342; AAC03542.1; -
DR HSSP; P01375; IAGM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
SQ SEQUENCE 157 AA; 17380 MW; D13448222679F20 CRC64;

Query Match
Best Local Similarity 7.9%; Score 133; DB 4; Length 157;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAQPPAHLTINAASIPSGSHKVTLSWYHDKGAKISN-MTSLNGKLRVNODGYIYLA 217
Db 8 PSDKPPAVHVAN---PQAEGL---QWLNRRANALLANGVELRDNLVVPSEGLYIYS 60

QY 218 NICEFRHETSGSVPTDYQLQ-----MVYVVK-----TSIKIPSSHNLKMGSTKNWSG 265
Db 61 QVLFK----GQCCPSTHLLTHTISRIAVSYQTKVNLISAISPCQRETPRGAERKPW-- 114

QY 266 NSEHFYSINVGFFKLKLRAGEEISIOVSNPSLID-PDQDATYFG 308
Db 115 -----YEPYLGGVFQKGRDLSAEINRPDYLDFAESGVYFG 153

RESULT 7
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097543
ID 097543 PRELIMINARY; PRT; 149 AA.
AC 097543;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nancyrae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RT Identification, cloning and sequencing of different interleukin genes in 4 Aotus species.
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014513; AAD01539.1; -
DR HSSP; P01375; WTSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFA8A CRC64;

Query Match
Best Local Similarity 7.9%; Score 132; DB 6; Length 149;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAQPPAHLTINAASIPSGSHKVTLSWYHDKGAKISN-MTSLNGKLRVNODGYIYLA 217
Db 1 PSDKPPAVHVAN---PQAEGL---QWLNRRANALLANGVELRDNLVVPSEGLYIYS 53

QY 218 NICEFRHETSGSVPTDYQLQ-----MVYVVK-----TSIKIPSSHNLKMGSTKNWSG 265
Db 54 QVLFK----GQCCPSTHLLTHTISRIAVSYQTKVNLISAISPCQRETPRGAERKPW-- 107

QY 266 NSEHFYSINVGFFKLKLRAGEEISIOVSNPSLID-PDQDATYFG 308
Db 108 -----YEPYLGGVFQKGRDLSAEINRPDYLDFAESGVYFG 146

RESULT 8
QY 09ERG6 PRELIMINARY; PRT; 217 AA.
AC 09ERG6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor necrosis factor genes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; RAG30264.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
```

Db 114 ---YPIYLGVGFQLEKGRDLRLSAEAVNHPKYLDFAESSGQVYFG 152

RESULT 10
ID Q97538 PRELIMINARY; PRT; 149 AA.
AC O97538
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patartoyo M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species".
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF014508; AAD01534.1;
DR HSP; P01375; 4TSV;
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149
FT NON_TER 149
SQ SEQUENCE 149 AA; 16415 MW; 86FlB9BCED165689 CRC64;

Query Match 7.8%; Score 131; DB 6; Length 149;
Best Local Similarity 24.4%; Pred. No. 0.00084;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps

QY 159 PPAQFAHLTINAAIPSGSHKVTLSSWYHDSGWAKISN-MTSLNGKLVRNQDGYLYA 217
Db 1 PSDKPVAHVAN-----PDAEGQL---OWLNRANALLANGVELRDVLVPVSGGLDYVS 53
QY 218 NICFRHETSGVPTDYIQL-----MVYVK-----TSIKIPSSHNLKMGSTKNWSG 265
Db 54 QVLFK----GCCPSTFMLLTHSIRIAVSQAQVNLISAISKPCQRETPRGATNPW-- 107
QY 266 NSEHFYSINVGGFKLRAGEISIQVSNPSLLD-PQQDATYFG 308
Db 108 -----YEPIYLGVGFEKGRDLRSABINLPDYLDLAESGOVYFG 146

RESULT 11
ID Q9TTG8 PRELIMINARY; PRT; 149 AA.
AC Q9TTG8
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA
OS Aotus nigriceps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patartoyo M.E.;
RT "Aotus nigriceps gene for TNF alpha";
RL Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF097328; AAF21303.1;
FT NON_TER 1
FT NON_TER 149
FT NON_TER 149
SQ SEQUENCE 149 AA; 16415 MW; 86FlB9BCED165689 CRC64;

Query Match 7.9%; Score 131.5; DB 11; Length 156;
Best Local Similarity 24.4%; Pred. No. 0.00081;
Matches 39; Conservative 27; Mismatches 61; Indels 35; Gaps 6;

QY 162 QPPAHLTINAAIPSGSHKVTLSSWYHDSGWAKISN-MTSLNGKLVRNQDGYLYANIC 220
Db 11 KPVAHVANAQAEQ-----LEWLORANALLANGDLNNLVLPADGLYLYSVQL 63
QY 221 FRHETSGVPTDYIQLMYYVVK-----TSIKIPSSHNLKMGSTKNWSGNS 267
Db 64 FK-----GLRSCNCELTHTVSRIVASYEDKVNLSAISKAISKPCQRETPQGAEAPW----- 113
QY 268 EFHFYSINVGGFKLRAGEISIQVSNPSLLD-PQQDATYFG 308

Ffam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
NON_TER 1
NON_TER 217
SEQUENCE 217 AA; 23964 MW; D6F90C74COB3021F CRC64;

Query Match 7.9%; Score 132; DB 11; Length 217;
Best Local Similarity 24.3%; Pred. No. 0.0011;
Matches 46; Conservative 31; Mismatches 68; Indels 44; Gaps 8;

QY 133 IVGPQRFCAGP-----AMWGSWLDVAQRGEAPQPFAPHAFLINAASIPSGSHKVTL- 184
Db 47 VIGPQERFPNNPLPIIGSMQTLTRSSONSDD-KPVARVVAN-----HQVDQL 97
Y 185 SWYHDGWNKISN-MTSLNGKLVRNQDGYLYANICFRHETSGVPTDYIQLMYYVVK 243
Db 98 EWLSRRANALLANGMDLNQVLPADGLYLYSVQLFKGGCSNY-----LLHTVS 151
QY 244 -----TSIKIPSSHNLKMGSKNSGSEPHFYINSVGGFFKLAGEIS 290
Db 152 RFNVSTEDKVNLSAISKAISKPCKETPESELKPW-----YEPIYLGVGFEKGRDLRLSA 204
QY 291 QVSNPSLLD 299
Db 205 EVNLPKYLD 213

RESULT 9
ID Q91ZL4 PRELIMINARY; PRT; 156 AA.
AC Q91ZL4
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-NAR-2002 (TREMBlrel. 20, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OX Sigmodon.
RN [1]
RP SEQUENCE FROM N.A.
RA Blanco J.C., Pietneva L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons".
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF421388; AAL18818.1;
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C826E4 CRC64;

Query Match 7.9%; Score 131.5; DB 11; Length 156;
Best Local Similarity 24.4%; Pred. No. 0.00081;
Matches 39; Conservative 27; Mismatches 61; Indels 35; Gaps 6;

QY 162 QPPAHLTINAAIPSGSHKVTLSSWYHDSGWAKISN-MTSLNGKLVRNQDGYLYANIC 220
Db 11 KPVAHVANAQAEQ-----LEWLORANALLANGDLNNLVLPADGLYLYSVQL 63
QY 221 FRHETSGVPTDYIQLMYYVVK-----TSIKIPSSHNLKMGSTKNWSGNS 267
Db 64 FK-----GLRSCNCELTHTVSRIVASYEDKVNLSAISKAISKPCQRETPQGAEAPW----- 113
QY 268 EFHFYSINVGGFKLRAGEISIQVSNPSLLD-PQQDATYFG 308

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DR HSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 149
SO SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match
Best Local Similarity 24.4%; Score 131; DB 6; Length 149;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

Qy 159 PEAQPAHLTINAAIPSGSHKVLSSWYHGRGAKISN-MTSLNGKLRVNDGFFYLYA 217
Db 1 PSDKPVAHVAN---PQAEGL---QWLNRRANALLANGVELRONQLVVPSEGLYLYS 53

218 NICFRHETSGVPTDYQL-----MYVVK-----TSIKIPSHNLKMGSTKNWSG 265
54 QVLFK-----GQCPTFMLLTHSIRIAVSYQAKVNLSSAIKSPQOREPFRGAKTNPW-- 107
266 NSEPFYSINVGFFKLRAAGEISIQVSNPSLLD-PDQDATYFG 308
108 -----YEPYLGGVFQLEKGRDLRSALINLPDYLDIAESQVYFG 146

RESULT 12
ID 070332 PRELIMINARY; PRT; 216 AA.
AC 070332;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN;
RX MEDLINE-98234044; PubMed-9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
FT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis."
L Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046215; AAC40100.1; -.
DR HSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 216
SO SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match
Best Local Similarity 24.7%; Score 130; DB 11; Length 216;
Matches 46; Conservative 29; Mismatches 71; Indels 40; Gaps 8;

Qy 133 IVGPORFSGAPAMGSGWLDV-----AORCKPEAQPAHLTINAAIPSGSHKVTLS-SWY 187
Db 47 VIGPQREKFPNIGSGQTLTLRSSSSQNDKPKGVHVVAN-----HQVEQLEWL 98

us-09-787-126-4.rspt
Qy 188 HDRGAKISN-MTSLNGKLRVNDGFFYLYANICFRHETSGVPTDYQLQMLVYVVK--- 243
Db 99 SHRANALLANGSLKDQNLVVPADGLYLYVSOYLER-----GQCPSYV-LLTHVSR 152
Qy 244 -----TSIKIPSHNLKMGSTKNWSGSEFHYFYSINVGFFKLRAAGEISIQVS 293
Db 153 VSYEDNVNLLSAIKSPCKPTEPEGEELPW-----YEPYLGGVFQLEKGRDLRSAL 205
Qy 294 NPSLLD 299
Db 206 LPKYLD 211

RESULT 13
Q9BEC5 PRELIMINARY; PRT; 217 AA.
ID Q9BEC5
AC Q9BEC5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tenrec ecaudatus (tailess tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.
OX NCBI_TaxID=94439;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286826; CAC28538.1; -.
DR HSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 217
SO SEQUENCE 217 AA; 23845 MW; 1C5013E9B77B54A CRC64;

Query Match
Best Local Similarity 24.0%; Score 127.5; DB 6; Length 217;
Matches 49; Conservative 29; Mismatches 51; Indels 75; Gaps 10;

Qy 133 IVGPORFSGAPAMGSGWLDVVAORCKPEAQ-----PFAHLTINAAIPSGSHK 180
Db 46 VIGPQREKFPNIGSGQTLTLRSSSSRLSDKPVAVHW---ASTQDEGQLK 95
Qy 181 VTLSSWYHGRGW-AKISNMTLSN-----GKLRVNDGFFYLYANICFRHETSGVPTD 233
Db 96 -----WVSRVANALLDNVQLDNLVPLDGLYLYVQLVFGPCGCHGT----- 140
Qy 234 YLQMLVYVVKT-----SIKIPSHNLKMGSTKNWSGSEFHYFYSIN 275
Db 141 -----YVLTHTVSVRIASVQAKVNLSSAIKTPCHRETPESETKPW-----YEPY 187
Qy 276 VGGFFKLRAAGEISIQVSNPSLLD 299
Db 188 LGGVFQLEKGRDLRSALINLPNYLD 211

RESULT 14
Q9BEG1 PRELIMINARY; PRT; 217 AA.
ID Q9BEG1
AC Q9BEG1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)

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01-JUN-2001 (Tremblrel. 17, Last sequence update)
01-DEC-2001 (Tremblrel. 19, Last annotation update)
Tumor necrosis factor (Fragment).
TNFA.
OS Bradypus tridactylus (Pale-throated three-toed sloth).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Bradypodidae; Bradypus.
OX NCBI_TaxID=9354;
RN [1]
SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT *Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.*
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286827; CAC28513.1; -
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
JR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23655 MW; A7056710B6238074 CRC64;
Query Match 7.6%; Score 126.5; DB 6; Length 217;
Best Local Similarity 25.0%; Pred. No. 0.0035;
Matches 47; Conservative 33; Mismatches 65; Indels 43; Gaps 10;
QY 133 IVGPQSGAPAMGGWNL--DVAQRK-----PEAQFAHLTINAASIPSGSHKVTLS 185
DB 46 VIGPQEEQFRGGLHPVNPPLAQTLRSSR--TPSDKPVAVHVN-----PQAGQL---Q 95
QY 186 WYDRGWAKISN-MTSLNGKLRVNDGFFYLYANICFRHETSGSVPTDYQLMAYVVK- 243.
DB 96 WLSRRANALLANGVELTDNQLVPSDGLYLYSQVLFK-GGCGFSTPV----LTHVNR 150
QY 244 -----TSIKIPSSHNLKMGSTKNWGNSEFFHYSINVGFFKLRAGEEISIQ 291
DB 151 FAVSYQTKVNLSSAIKSPCQRETPEGTGKPV-----YEPYLGGVFQLDKGRLSAE 203
QY 292 VSNFSLLD 299
DB 204 INLPDYLD 211
RESULT 15
QYBEGO QYBEGO PRELIMINARY; PRF; 217 AA.
AC QYBEGO;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxID=84074;
RN [1]
SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT *Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.*
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286828; CAC28514.1; -
DR HSSP; P01375; IABM.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23753 MW; F760E887F6C29EBB CRC64;
Query Match 7.6%; Score 126.5; DB 6; Length 217;
Best Local Similarity 24.9%; Pred. No. 0.0035;
Matches 46; Conservative 33; Mismatches 69; Indels 37; Gaps 10;
QY 133 IVGPQ--REFSGA--PAMMEGSLDVAQRKPEAQFAHLTINAASIPSGSHKVTLSWY 187
DB 46 VIGPQEEQFRGGLHPVNPPLAQTLRSSR--TPSDKPVAVHVN-----PQAGQL---QWL 97
QY 188 HDRGWAKISN-MTSLNGKLRVNDGFFYLYANICFRHETSGSVPTDYQL-----M 238
DB 98 SRRANALLANGVELTDNQLVPSDGLYLYSQVLFK-----GQCGPSARVLLTHVNRPAV 153
QY 239 VYVVK-----TSIKIPSSHNLKMGSTKNWGNSEFFHYSINVGFFKLRAGEEISIQVSN 294
DB 154 SYQTKVNLSSAIKSPCQRETPEGTGKPV-----YEPYLGGVFQLDKGRLSAEINL 206
QY 295 PSLLD 299
DB 207 PEYLD 211
Search completed: April 16, 2003, 12:20:03
Job time : 30 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1675	100.0	316	2	US-08-842-842-7	Sequence 7, Appl
2	1675	100.0	316	4	US-08-989-362-2	Sequence 2, Appl
3	1675	100.0	316	4	US-09-052-521C-2	Sequence 2, Appl
4	1554	92.8	294	3	US-08-996-139-11	Sequence 11, Appl
5	1554	92.8	294	4	US-08-995-659-11	Sequence 11, Appl
6	1554	92.8	294	4	US-09-215-649A-11	Sequence 11, Appl
7	1554	92.8	294	4	US-09-577-780-11	Sequence 11, Appl
8	1417.5	84.6	317	3	US-08-996-139-13	Sequence 13, Appl
9	1417.5	84.6	317	4	US-08-995-659-13	Sequence 13, Appl
10	1417.5	84.6	317	4	US-09-215-649A-13	Sequence 13, Appl
11	1417.5	84.6	317	4	US-09-052-521C-4	Sequence 4, Appl
12	1417.5	84.6	317	4	US-09-577-780-13	Sequence 13, Appl
13	258.5	15.4	279	4	US-09-072-993C-3	Sequence 3, Appl
14	258.5	15.4	281	1	US-08-670-334-2	Sequence 2, Appl
15	258.5	15.4	281	3	US-08-584-031-1	Sequence 1, Appl
16	258.5	15.4	281	3	US-08-780-496-1	Sequence 1, Appl
17	258.5	15.4	281	4	US-08-883-086-10	Sequence 10, Appl
18	258.5	15.4	281	4	US-09-320-424-2	Sequence 2, Appl
19	258.5	15.4	281	4	US-09-333-593A-6	Sequence 6, Appl
20	258.5	15.4	281	4	US-09-157-864-11	Sequence 11, Appl
21	258.5	15.4	281	5	PCR-US96-10895-2	Sequence 2, Appl
22	244	14.6	291	1	US-08-670-354-6	Sequence 6, Appl
23	244	14.6	291	4	US-09-320-424-6	Sequence 6, Appl
24	244	14.6	291	5	PCR-US96-10895-6	Sequence 6, Appl
25	240	14.3	256	4	US-09-320-424-13	Sequence 13, Appl
26	236	14.1	253	4	US-09-320-424-11	Sequence 11, Appl
27	229.5	13.7	177	4	US-09-105-343A-7	Sequence 7, Appl

[illegible]

Query Match	100.0%	Score 1675;	DB 4;	Length 316;
Best Local Similarity	100.0%	Pred. No. 4.7e-157;		
Matches 316;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MRRASRDYGVKYLRSSEMGSGVPHEGPHLPAPAPAPAPPAAASRSMFLALIGLGGQ	60	
Db	1	MRRASRDYGVKYLRSSEMGSGVPHEGPHLPAPAPAPAPPAAASRSMFLALIGLGGQ	60	
Qy	61	VVCSIALFLYFRAQMDPNRISEDSSTHCFYRILRLHENAGLQDSTLSEEDTLPDSCRRMQ	120	
Db	61	VVCSIALFLYFRAQMDPNRISEDSSTHCFYRILRLHENAGLQDSTLSEEDTLPDSCRRMQ	120	
Qy	121	AFQGAOVKEIQLHIVGPORFSGAPAMMEGSLDVAQKRGKPEAOPFAHLTNAASIPSGSHK	180	
Db	121	AFQGAOVKEIQLHIVGPORFSGAPAMMEGSLDVAQKRGKPEAOPFAHLTNAASIPSGSHK	180	
Qy	181	VTLSWSYHDRGWAKISNMTLSNGLKRVNQDGFYLLYANICFRHHETSGSVPTDYLQMWY	240	
Db	181	VTLSWSYHDRGWAKISNMTLSNGLKRVNQDGFYLLYANICFRHHETSGSVPTDYLQMWY	240	
Qy	241	VVKTSIKIPSSHNLMLKGGSTKNNSGNSEHFYSINVGGFFKLRAGEISIQVSNPISLDP	300	
Db	241	VVKTSIKIPSSHNLMLKGGSTKNNSGNSEHFYSINVGGFFKLRAGEISIQVSNPISLDP	300	
Qy	301	QDQATYFQAFKQVQDID	316	
Db	301	QDQATYFQAFKQVQDID	316	

RESULT 4
US-08-996-139-11
: Sequence 139, Application US/08996139
: Patent No. 601729
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene

```

: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/996,139
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-996-139-11

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Query Match 92.8%; Score 1554; DB 3; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 23 GYPHEGLHPAPSAPAPAPPAAASRMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 82
Jb 1 GYPHEGLHPAPSAPAPAPPAAASRMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 60
Qy 83 DSTHCFYRLRLHENAGLDSTLESEDYLPDSCRMKAQFQAVOKELQHVGPORFSGA 142
Db 61 DSTHCFYRLRLHENAGLDSTLESEDYLPDSCRMKAQFQAVOKELQHVGPORFSGA 120
Qy 143 PAMBGSLDVAQRKPEAQPFPAHLTINAAISPGSHKVTLSWYHDSRGWAKISNMTLSN 202
Db 171 PAMBGSLDVAQRKPEAQPFPAHLTINAAISPGSHKVTLSWYHDSRGWAKISNMTLSN 180
Qy 203 GKLRVNDGFFYLNYANICFRHHETSGSVPTDYQLMVTYVVKTSIKIPSSHNLMKGGSTKN 262
Db 181 GKLRVNDGFFYLNYANICFRHHETSGSVPTDYQLMVTYVVKTSIKIPSSHNLMKGGSTKN 240
Qy 263 WSGNSEFHYSINVGCFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 316
Db 241 WSGNSEFHYSINVGCFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 294

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RESULT 5
US-08-995-659-11
: Sequence 11, Application US/08995659
: Patent No. 6242213
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.

```

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: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/995,659
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-995-659-11

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Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 23 GYPHEGLHPAPSAPAPAPPAAASRMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 82
Db 1 GYPHEGLHPAPSAPAPAPPAAASRMFLALIGLGQVVCISIALFLYFRAQMDPNRISE 60
Qy 83 DSTHCFYRLRLHENAGLDSTLESEDYLPDSCRMKAQFQAVOKELQHVGPORFSGA 142
Db 61 DSTHCFYRLRLHENAGLDSTLESEDYLPDSCRMKAQFQAVOKELQHVGPORFSGA 120
Qy 143 PAMBGSLDVAQRKPEAQPFPAHLTINAAISPGSHKVTLSWYHDSRGWAKISNMTLSN 202
Db 121 PAMBGSLDVAQRKPEAQPFPAHLTINAAISPGSHKVTLSWYHDSRGWAKISNMTLSN 180
Qy 203 GKLRVNDGFFYLNYANICFRHHETSGSVPTDYQLMVTYVVKTSIKIPSSHNLMKGGSTKN 262
Db 181 GKLRVNDGFFYLNYANICFRHHETSGSVPTDYQLMVTYVVKTSIKIPSSHNLMKGGSTKN 240
Qy 263 WSGNSEFHYSINVGCFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 316
Db 241 WSGNSEFHYSINVGCFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 294

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RESULT 6

Query Match	84.6%	Score 1417.5	DB 3	Length 317
Best Local Similarity	84.3%	Pred. No. 1.1e-131		
Matches 268	Conservative 16	Mismatches 31	Indels 3	Gaps 2
Qy	1	MRRASRDYGYLRSSEEMSGSGVPYHGGLHPAPSAPAPAPPAAASRSMFTALLGLGLGQ	60	
Db	1	MRRASRDYKYLRSSEEMSGGPGAPHGGLP-L-APPFAPHPQPPAASRSMFVALLGLGLGQ	59	
Qy	61	VVCSIALFLYFRAQMDPNRISEDSHTCFYIRILRLHLENAGLQDSTLESDT--LPDSCRRM	118	
Db	60	VVCSVALFFYFRAQMDPNRISEDCGTHCIYIRILRLHENADFQDTTLESDQTKLIPDSCRR	119	
Qy	119	KQAPQGAQVQELQIIVGQRFPSGAPAMWESWLDVQORGPFAQPFAPHLTINAASTPSGS	178	
Db	120	KQAPQGAQVQELQIIVGQSHIRAEKAWDGSWLDLAKRSLEAQPFAPHLTINATDIPSGS	179	
Qy	179	HKVTLSSWYHDGRWAKLSNMTLSNGKLRYNDGFPYLYIYANICFRHHETSGGSPDYLIQLM	238	
Db	180	HKVSLSSWYHDGRWAKLSNMTFSNGKLRYNDGFPYLYIYANICFRHHETSGDLAYEYLIQLM	239	
Qy	239	VYVYKTSIKIPSSHNLMKGGSSTKNWGSNSEPHFYSINVGGFFKLRAAGEETISIOVNSPLL	298	

	Query Match	84.6%	Score 1417.5;	DB 4;	Length 317;
	Best Local Similarity	84.3%;	Pred. No. 1.le-131;		
	Matches 268;	Conservative 16;	Mismatches 31;	Indels 3;	Gaps 2;
Qy	1 MRRASRDYCKYLRSSEEMSGPGVPHGCPHLPAPASAPAPAPPAAASRSMFALLGLGLQG	60			
Dd					
Qy	1 MRRASRDYTKYLRSEEMGGGFGPAGHEGPLH - APPPPAPHQPAPAAASRSMFALLGLGLQG	59			
Dd					
Qy	61 VVCSTALFLYFAOAMDPNRISEDSTHCFFYRLIRLHENAGLDSTLESDET -- LPDSCRMM	118			
Dd					
Qy	60 VCVSVALFFYFAOAMDPNRISEDGTHCYIRLIRLHENADFOOTWLESQDTKLIIPDSCRRI	119			
Dd					
Qy	119 KOAFQGVQVKELQHVIGVPQRSGAPAMNEGSLWDVAQRKPCEAOPFAHLITINAAISIPGS	178			

Db 120 KOAFQAVOKELQHVGSQHIAERAKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 179
 QY 179 HKVTLSSWYHDSRGWAKISNMTLSNGLRVNODGFYLLYANICFRHETSGSVPTDYQLQM 238
 Db 180 HKVTLSSWYHDSRGWAKISNMTLSNGLRVNODGFYLLYANICFRHETSGDLATEYLQM 239
 QY 239 VYVTKTSIKIPSSHLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVSNPSLL 298
 Db 240 VYVTKTSIKIPSSHLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYFGAFKVDID 316
 Db 300 DPQDATYFGAFKVDID 317

RESULT 10

US-09-215-649A-13
 ; Sequence 13, Application US/09215649A
 ; Patent No. 6271349

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
 Galibert, Laurent
 Maraskovsky, Eugene
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/215,649A
 FILING DATE: 17-Dec-1998
 CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/996,139
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-215-649A-13

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
 Db 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPPPAASRSMFLALLGLGLGQ 59

QY 61 VVCSTALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESDT--LPDSCRRM 118
 Db 60 VVCSTALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESDT--LPDSCRRM 119
 QY 119 KOAFQAVOKELQHVGSQHIAERAKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 178
 Db 120 KOAFQAVOKELQHVGSQHIAERAKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 179
 QY 179 HKVTLSSWYHDSRGWAKISNMTLSNGLRVNODGFYLLYANICFRHETSGSVPTDYQLQM 238
 Db 180 HKVTLSSWYHDSRGWAKISNMTLSNGLRVNODGFYLLYANICFRHETSGDLATEYLQM 239
 QY 239 VYVTKTSIKIPSSHLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVSNPSLL 298
 Db 240 VYVTKTSIKIPSSHLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYFGAFKVDID 316
 Db 300 DPQDATYFGAFKVDID 317

RESULT 11

US-09-052-521C-4
 ; Sequence 4, Application US/09052521C
 ; Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.
 TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 FILE REFERENCE: A-451brv
 CURRENT APPLICATION NUMBER: US/09/052,521C
 CURRENT FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 08/880,855
 PRIOR FILING DATE: 1997-06-23
 PRIOR APPLICATION NUMBER: 08/842,842
 PRIOR FILING DATE: 1997-04-16
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 317
 TYPE: PPT
 ORGANISM: Human
 US-09-052-521C-4

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
 Db 1 MRRASRDYCKYLRSSEMGSGPGVHEGPHLPAPAPPPAASRSMFLALLGLGLGQ 59
 QY 61 VVCSTALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESDT--LPDSCRRM 118
 Db 60 VVCSTALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLDSTLESDT--LPDSCRRM 119
 QY 119 KOAFQAVOKELQHVGSQHIAERAKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 178
 Db 120 KOAFQAVOKELQHVGSQHIAERAKAMVDGSLDLAKRSKLEAQPFALHTINATDIPSGS 179
 QY 179 HKVTLSSWYHDSRGWAKISNMTLSNGLRVNODGFYLLYANICFRHETSGSVPTDYQLQM 238
 Db 180 HKVTLSSWYHDSRGWAKISNMTLSNGLRVNODGFYLLYANICFRHETSGDLATEYLQM 239
 QY 239 VYVTKTSIKIPSSHLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIQVSNPSLL 298
 Db 240 VYVTKTSIKIPSSHLMKGGSTKNWSEHFFYSINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYFGAFKVDID 316
 Db 300 DPQDATYFGAFKVDID 317

RESULT 12


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RESULT 15
US-08-584-031-1
: Sequence 1, Application US/08584031A
: Patent No. 6030945
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: TITLE OF INVENTION: APO-2 LIGAND
: FILE REFERENCE: 11669.22US03
: CURRENT APPLICATION NUMBER: US/08/584,031A
: CURRENT FILING DATE: 1996-01-09
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 281
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-584-031-1

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GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 12:18:42 ; Search time 14.5 seconds
(without alignments)
1647.861 Million cell updates/sec

Title: US-09-787-126-4
Perfect score: 1675
Sequence: 1 MRRASRDYKYLRSSEMGs.....LLDPQDQATYFGAKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Marched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_PEP.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB_PEP.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUB_PEP.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB_PEP.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB_PEP.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB_PEP.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB_PEP.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	9	US-10-017-910-4
2	1675	100.0	316	9	US-10-105-057-2
3	1554	92.8	294	9	US-09-877-650-11
4	1554	92.8	294	10	US-09-871-856-11
5	1417.5	84.6	317	9	US-09-877-650-13
6	1417.5	84.6	317	10	US-09-813-329-7
7	1417.5	84.6	317	10	US-09-871-856-13
8	1101	65.7	245	9	US-10-017-910-2
9	855	51.0	160	9	US-09-779-050A-14
10	768	45.9	160	9	US-09-779-050A-15
11	496	29.6	109	10	US-09-911-777-8
12	258.5	15.4	279	12	US-10-066-209-3
13	258.5	15.4	281	8	US-08-916-625B-6
14	258.5	15.4	281	9	US-08-971-317A-8
15	258.5	15.4	281	9	US-10-001-054-54
16	258.5	15.4	281	9	US-10-093-766-54
17	258.5	15.4	281	9	US-10-174-654-11
18	258.5	15.4	281	9	US-10-151-882-41
19	258.5	15.4	281	10	US-09-813-329-17

20	258.5	15.4	281	10	US-09-193-663-8	Sequence 8, Appl
21	258.5	15.4	281	10	US-09-934-465-1	Sequence 1, Appl
22	258.5	15.4	281	12	US-10-039-785-66	Sequence 66, Appl
23	258.5	15.4	281	12	US-10-011-125-4	Sequence 4, Appl
24	244	14.6	291	9	US-10-017-910-6	Sequence 6, Appl
25	234	14.0	296	9	US-10-185-425-5	Sequence 5, Appl
26	232	13.9	246	10	US-09-855-540A-13	Sequence 13, Appl
27	230.5	13.8	168	10	US-09-900-530A-10	Sequence 10, Appl
28	229.5	13.7	166	9	US-09-779-050A-16	Sequence 16, Appl
29	225	13.4	172	9	US-09-779-050A-17	Sequence 17, Appl
30	220.5	13.2	164	12	US-10-116-378-29	Sequence 29, Appl
31	183	10.9	278	10	US-09-246-129B-6	Sequence 6, Appl
32	183	10.9	278	10	US-09-899-059-6	Sequence 6, Appl
33	182	10.9	279	8	US-10-017-910-5	Sequence 5, Appl
34	181	10.8	279	8	US-08-971-317A-4	Sequence 4, Appl
35	181	10.8	279	10	US-09-193-663-4	Sequence 4, Appl
36	176	10.5	87	10	US-09-880-457-4	Sequence 4, Appl
37	176	10.5	94	10	US-09-880-457-5	Sequence 5, Appl
38	176	10.5	95	9	US-10-237-884-82	Sequence 82, Appl
39	176	10.5	95	9	US-10-230-163-82	Sequence 82, Appl
40	176	10.5	95	9	US-10-218-631-82	Sequence 82, Appl
41	176	10.5	95	9	US-10-230-338-82	Sequence 82, Appl
42	176	10.5	95	9	US-10-230-414-82	Sequence 82, Appl
43	176	10.5	95	9	US-10-216-159A-82	Sequence 82, Appl
44	176	10.5	95	10	US-09-880-457-6	Sequence 6, Appl
45	173.5	10.4	281	8	US-08-971-317A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-017-910-4
; Sequence 4, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph

TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCOD METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/447,035

FILING DATE: 1999-11-22

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-200

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

DB 01 DSIHCFIRIKRHNADLQDSISESE

QY	143	PAMMEGSLWDAVORGPEAOPFAHLTINAASIPSGSHKVTLSWSYHRCGAKISNMTLSN	202
Db	121	PAMMEGSLWDAVORGPEAOPFAHLTINAASIPSGSHKVTLSWSYHRCGAKISNMTLSN	180
QY	203	GKLRVNDGFPYLLYANICFRHHETSGSVPTDYLLQLMYYVVKTSIKIPSSHNLMMKGSTKN	262
Db	181	GKLRVNDGFPYLLYANICFRHHETSGSVPTDYLLQLMYYVVKTSIKIPSSHNLMMKGSTKN	240
QY	263	WSGNSRPHFYSINVGPFKKLRACEEETSIOVNSPLDLPQDATYFGAFKVQDID	316
Db	241	WSGNSRPHFYSINVGPFKKLRACEEETSIOVNSPLDLPQDATYFGAFKVQDID	294

RESULT 4

US-09-871-856-11
; Sequence 11, Application US/09871856
; Patent No. US20020081720A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>

Query Match 92.8%; Score 1554; DB 10; Length 294;
Best Local Similarity 99.7%; Pred. No. 4.5e-129;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	23	GVP	H	E	G	L	H	P	A	P	A	P	P	A	S	R	S	M	F	A	L	L	G	I	G	I	G	O	V	C	S	T	A	L	F	L	F	R	A	O	M	D	N	R	I	S	E	82											
Db	1	GVP	H	E	G	L	H	P	A	P	A	P	A	P	A	S	R	S	M	F	A	L	L	G	I	G	I	G	O	V	C	S	T	A	L	F	L	F	R	A	O	M	D	N	R	I	S	E	60										
Qy	83	D	S	T	H	C	F	Y	R	I	L	R	L	H	E	N	A	G	L	O	S	T	L	E	S	E	D	T	L	P	D	S	C	R	R	K	M	K	A	P	Q	G	A	V	O	K	E	L	H	I	V	G	P	Q	R	F	S	G	142
Db	61	D	S	T	H	C	F	Y	R	I	L	R	L	H	E	N	A	G	L	O	S	T	L	E	S	E	D	T	L	P	D	S	C	R	R	K	M	K	A	P	Q	G	A	V	O	K	E	L	H	I	V	G	P	Q	R	F	S	G	120

Qy	143	PAMMEGSLWDAORGP	PEAQPFAHL	TINAAS	TPSGSHKVTLS	SWHDCGAKISNKTLS	202
Db	121	PAMMEGSLWDAORGP	PEAQPFAHL	TINAAS	TPSGSHKVTLS	SWHDCGAKISNKTLS	180
Qy	203	GKLRVNDGFPYLLY	ANICFRH	HETSGSVPTDY	LQLM	VYVYVTSIKIPSSHNLMKGGSTKN	262
Db	181	GKLRVNDGFPYLLY	ANICFRH	HETSGSVPTDY	LQLM	VYVYVTSIKIPSSHNLMKGGSTKN	240
Qy	263	WSGNSPEHFTYS	INVGGFFKLR	AGEEISIOV	SNPSLDPQD	ATYFGAFKVQDID	316
Db	241	WSGNSPEHFTYS	INVGGFFKLR	AGEEISIOV	SNPSLDPQD	ATYFGAFKVQDID	294

5. **RESULTS**

```

US-09-877-650-13
Sequence 13, Application US/09877650
Patent No. US20020169117A1
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Maraskovsky, Eugene
Galibert, Laurent
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
FILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2852-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-650-13

```

Query Match	84.6%	Score 1417.5;	DB 9;	Length 317;
Best Local Similarity	84.3%	Pred. No. 5.2e-117;		
Matches 268;	Conservative	16;	Mismatches 31;	Indels 3;
				Gaps 2;

QY	1	MRRSRDYGYKYLRSSEMGSGPGVPHGPHLPAPAPAPAPPAAASRSFVALLIGLGLGQ	60
Db	1	MRRSRDYTKYLRSSEMGSGPGAPHEGPHL-APPAPHPQPPAAASRSFVALLIGLGLGQ	59
QY	61	VVCSIALFLFRAQMDPNRISSESTCFYKILRLHFNAGLQDLSLEDTI--LPDSCRRM	118

Db 60 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDQTTLESQDTKLIPDSMRI 119
QY 119 KQAFQAVOKELQHVGPQFSCAPAMGSGWLDVAQRKPEAOPFAHLTINAAISIPSGS 178
Db 120 KQAFQAVOKELQHVGSQHRAERKAWVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
QY 179 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYILRLHENAGLDSTLESDT--LPDSCRRM 238
Db 180 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYILRLHENAGLDSTLESDT--LPDSCRRM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLRAGEEISIQVNSPLL 298
Db 240 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLRAGEEISIQVNSPLL 299
QY 299 DPQDATYFAGFKVRDID 316
Db 300 DPQDATYFAGFKVRDID 317

RESULT 6

US-09-813-329-7
Sequence 7, Application US/09813329
Patent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patent version 3.0
SEQ ID NO 7
LENGTH: 317
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYKYLRSSEMGSGCPVHEGLHPAPAPAPPAAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEMGSGCPVHEGLHPAPAPAPPAAASRSMFLALLGLGLGQ 59
QY 61 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENAGLDSTLESDT--LPDSCRRM 118
Db 60 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENAGLDSTLESDT--LPDSCRRM 119
QY 119 KQAFQAVOKELQHVGPQFSCAPAMGSGWLDVAQRKPEAOPFAHLTINAAISIPSGS 178
Db 120 KQAFQAVOKELQHVGSQHRAERKAWVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
QY 179 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYILRLHENAGLDSTLESDT--LPDSCRRM 238
Db 180 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYILRLHENAGLDSTLESDT--LPDSCRRM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLRAGEEISIQVNSPLL 298
Db 240 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLRAGEEISIQVNSPLL 299
QY 299 DPQDATYFAGFKVRDID 316
Db 300 DPQDATYFAGFKVRDID 317

RESULT 7

US-09-871-856-13
Sequence 13, Application US/09871856
Patent No. US20020081720A1

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYKYLRSSEMGSGCPVHEGLHPAPAPAPPAAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEMGSGCPVHEGLHPAPAPAPPAAASRSMFLALLGLGLGQ 59
QY 61 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENAGLDSTLESDT--LPDSCRRM 118
Db 60 VVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENAGLDSTLESDT--LPDSCRRM 119
QY 119 KQAFQAVOKELQHVGPQFSCAPAMGSGWLDVAQRKPEAOPFAHLTINAAISIPSGS 178
Db 120 KQAFQAVOKELQHVGSQHRAERKAWVDGSLDLAKRSKLEAOPFAHLTINATDIPSGS 179
QY 179 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYILRLHENAGLDSTLESDT--LPDSCRRM 238
Db 180 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYILRLHENAGLDSTLESDT--LPDSCRRM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLRAGEEISIQVNSPLL 298
Db 240 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGFFKLRAGEEISIQVNSPLL 299
QY 299 DPQDATYFAGFKVRDID 316
Db 300 DPQDATYFAGFKVRDID 317

RESULT 8

US-10-017-910-2
; Sequence 2, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; MOLECULE TYPE: protein
; TYPE: amino acid
; LENGTH: 245 amino acids
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
JS-10-017-910-2

Query Match 65.7%; Score 1101; DB 9; Length 245;
Best Local Similarity 84.1%; Pred. No. 2.7e-89;
Matches 206; Conservative 14; Mismatches 23; Indels 2; Gaps 1;
QY 74 QMDPNRISDTHCFYRLRLHENAAGLDSTLESDT--LPDSCRRMKAQFQAVQKELQ 131
DB 1 QMDPNRISDTHCFYRLRLHENAAGLDSTLESDT--LPDSCRRMKAQFQAVQKELQ 60
QY 132 HIVGQRFSGAPAMMEGSLDVAORGPAPFAHLTINAAIPSGSHKVTLSWYHNRG 191
DB 61 HIVGSHIRAEKAMVDGSLDLAKSKLEAQPFAHLTINATDIPSGSHKVTLSWYHNRG 120
QY 192 WAKTSNMTLSNGLKRVNODGFFYLYANICFRHETSGVPTDYQLMVTYVTKTSIKIPSS 251
DB 121 WGISNMTFSNGLKRVNODGFFYLYANICFRHETSGDLATEYLQLMVTYVTKTSIKIPSS 180
QY 252 HNLKGGSTKWSGNSSEFFHSYINVGFFKLAGEEISQVSNPILDDPDQDATYFGAFK 311
DB 181 HNLKGGSTKWSGNSSEFFHSYINVGFFKLAGEEISQVSNPILDDPDQDATYFGAFK 240
QY 312 VQDID 316
DB 241 VRDID 245

RESULT 9

US-09-779-050A-14
; Sequence 14, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-14

Query Match 51.0%; Score 855; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 7e-68;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 157 GKPEAQPPAHLTINAAIPSGSHKVTLSWYHNRGAKISNMTLSNGLKRVNODGFFYLY 216
DB 1 GKPEAQPPAHLTINAAIPSGSHKVTLSWYHNRGAKISNMTLSNGLKRVNODGFFYLY 60
QY 217 ANICFRHETSGVPTDYQLMVTYVTKTSIKIPSSNLMKGGSTKWSGNSSEFFHSYIN 276
DB 61 ANICFRHETSGVPTDYQLMVTYVTKTSIKIPSSNLMKGGSTKWSGNSSEFFHSYIN 120
QY 277 GGFKLAGEEISQVSNPILDDPDQDATYFGAFKVDID 316
DB 121 GGFKLAGEEISQVSNPILDDPDQDATYFGAFKVDID 160

RESULT 10

US-09-779-050A-15
; Sequence 15, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-15

Query Match 45.9%; Score 768; DB 9; Length 160;
Best Local Similarity 89.9%; Pred. No. 3.2e-60;
Matches 143; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 158 KPEAQPPAHLTINAAIPSGSHKVTLSWYHNRGAKISNMTLSNGLKRVNODGFFYLY 217
DB 2 KLEAQPPAHLTINATDIPSGSHKVTLSWYHNRGAKISNMTLSNGLKRVNODGFFYLY 61
QY 218 NTCFRHETSGVPTDYQLMVTYVTKTSIKIPSSNLMKGGSTKWSGNSSEFFHSYIN 277
DB 62 NTCFRHETSGDLATEYLQLMVTYVTKTSIKIPSSHTLMKGGSTKWSGNSSEFFHSYIN 121

QY 278 GFFKLAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
Db 122 GFFKLAGEEISIEVSNPSLLDPDQDATYFGAFKVRDID 160

RESULT 11

US-09-911-777-8
; Sequence 8, Application US/09911777
; Patent No. US20020037852A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: APOTECH S.A.
; APPLICANT: BROWNING, Jeffrey
; APPLICANT: AMBROSE, Christine
; APPLICANT: MACKAY, Fabienne
; APPLICANT: TSCHOPP, Jurg
; APPLICANT: SCHNEIDER, Pascal
; TITLE OF INVENTION: BAPF, Inhibitors Thereof and Their Use
; TITLE OF INVENTION: in the Modulation of B-Cell Response
; FILE REFERENCE: A070 US
; CURRENT APPLICATION NUMBER: US/09/911,777
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/117,169
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 60/143,228
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: PCT/US00/01788
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-911-777-8

Query Match 29.6%; Score 496; DB 10; Length 109;
Best Local Similarity 68.5%; Pred. No. 1.7e-36;
Matches 98; Conservative 5; Mismatches 6; Indels 34; Gaps 2;

QY 160 EAQPFALHTNAASIPSGSHKVTLSWYHHRGWAKISNMTLSNKLKRVNODGYIYANI 219
Db 1 EAQPFALHTNATDIPSGSHKVSLSWYHHRGWGKISNM-----YANI 43
QY 220 CFRHETSGVPTDYQLQVMVYVTKSIKIPSSHNLMKGGTKWNSGSEHFYSINVGGF 279
Db 44 CFRHETSGDLATYQLQVMVYVTKSIKIP-----SEHFYSINVGGF 86

QY 280 FKLAGEEISIQVSNPSLLDPDQ 302
87 FKLAGEEISIEVSNPSLLDPDQ 109

RESULT 12

US-10-066-209-3
; Sequence 3, Application US/10066209
; Patent No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: US/10/066,209
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3

Query Match 15.4%; Score 258.5; DB 12; Length 279;
Best Local Similarity 26.4%; Pred. No. 4.9e-15;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

QY 43 PAASRSMFLALGLGQVVCISIALFLYFRAQMD--PNRISESTHCFYRILRLHENAGL 100
Db 8 PSLGQTCVLIVITVLLQSLCVATVYVFTNELKQMDKYSKSGIACF-----LKEDSY 62
QY 101 QDSTLESEDLPDSCRRMKOAFQAVOK-----ELQHVIGPQFSGAPAMM 146
Db 63 WDP--NDESGMNSPCMQVKWQLRQLVRKMLRTSEETISTVQEKQONISPL----- 111
QY 147 EGSMLDVAORKEPAQPFALHT-----INAAISPSGSHKVTL-----SSWYHDR-GWAKIS 196
Db 112 -----VREGRPORVA--AHITGRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFLS 163
QY 197 NMTLSNGKLRVNDQGFYLYANICFRHHETSGSVPTDYQLQVMVYVTKSIKIPSSHNLMK 256
Db 164 NLHLRNGELVIHEKGFYIYSQTYFRQEKENTKNDKQVQYIYKT-SYDPILLMK 222
QY 257 GGSTKMWNSGFHYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
Db 223 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAPLV 278

RESULT 13

US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Patent No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; INFORMATION FOR SEQ ID NO: 6:

PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100263
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/107783
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112420
PRIOR FILING DATE: 1998-12-15
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PRIOR FILING DATE: 2001-06-29

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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match      15.4%; Score 258.5; DB 9; Length 281;
Best Local Similarity 26.4%; Pred. No. 5e-15;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

Qy 43 PAASRMFLALLGLGQVVCISIALFLYFRAQMD--PNRISEDSHCHCFYRLRLHENAGL 100
Db 10 PSLGQTCVLIIVFTVLLQSLCAVAVTYFTNELKQMDKYKSGIACF-----LKEDDSY 64
/ 101 ODSTLESEDTLPDSCRRMKQAFQGAQVK-----ELQHVGPQRFSGAPAMM 146
Db 65 WDP--NDEESMNSPCWQVKNQURVRRKMLTSETISTVQEKQNNISPL----- 113
Qy 147 EGSWLDVAQGRKPEAQFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
Db 114 -----VREGRQRYA--AHITGTRSRNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
Qy 197 NMTLSNGKLVRNQDGFYLYXANICFRHETSGVPTDYQLMAYVYVYKTSIKIPSSHNLMK 256
Db 166 NLHLRNGELVIERKGFYIYTSQTYPRFQBEIKENTKNDKQMVQYIYKYT-SYPDPILLMK 224
Qy 257 GGSTRNWSGNSEFHEYSINVGGFFKLAGEEELISIOVSNPSLDDPDODATYFCAGKV 312
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
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Search completed: April 16, 2003, 12:21:51
Job time : 16.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:15:36 ; Search time 33.5 seconds
(without alignments)

1256.931 Million cell updates/sec

Title: US-09-787-126-6

Perfect score: 1675

Sequence: 1 MRRASRDYKYLSEEMGS.....LLDPDQDATYFGAFKVDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	1675	100.0	316 19	AAW83194 Human osteoprotegerin
2	1675	100.0	316 19	AAW83017 Osteoclastogenesis
3	1675	100.0	316 19	AAW59654 Amino acid sequenc
4	1675	100.0	316 20	AAV17874 Murine RANKL protei
5	1675	100.0	316 21	AAV91024 Mouse OBM protein
6	1675	100.0	316 21	AAV84418 Amino acid sequenc
7	1675	100.0	316 21	AAV84419 Amino acid sequenc
8	1675	100.0	316 23	AAU78289 Mouse TRANCE prote
9	1597	95.3	318 22	AAW82092 Rat osteoclast dif
10	1554	92.8	294 19	AAW69956 NF-kB receptor act

11	1554	92.8	294	19	AAW68292	NF-kB receptor act
12	1554	92.8	294	22	AAE08737	Murine receptor ac
13	1554	92.8	294	22	AAE04425	Murine receptor ac
14	1554	92.8	294	22	AAE01992	Murine RANKL (rece
15	1417.5	84.6	317	19	AAW83195	Human osteoprotege
16	1417.5	84.6	317	19	AAW69957	NF-kB receptor act
17	1417.5	84.6	317	19	AAW68293	NF-kB receptor act
18	1417.5	84.6	317	19	AAW84417	Amino acid sequenc
19	1417.5	84.6	317	22	AAE08738	Human receptor act
20	1417.5	84.6	317	22	AAE04426	Human full-length
21	1417.5	84.6	317	22	AAE01993	Human RANKL polye
22	1417.5	84.6	317	23	AAU78285	Human TRANCE prote
23	1417.5	84.6	317	23	AAU78285	Osteoclastogenesis
24	1409.5	84.1	317	19	AAW83018	Amino acid sequenc
25	1318	78.7	501	22	AAW84420	A murine OCIF-bind
26	1297	77.4	244	19	AAW83019	Osteoclastogenesis
27	1107	66.1	246	19	AAW83020	Human TRANCE. Hom
28	1101	65.7	245	20	AAU17873	Human PRO206 polyp
29	1100	65.7	244	23	AAU86148	Human TRANCE prote
30	1100	63.7	244	23	AAU78286	GlutathioneStransf
31	960	57.3	409	23	AAO17115	Murine GST-MODF fu
32	960	57.3	409	23	AAW49711	Amino acid sequenc
33	855	51.0	160	21	AAE08272	Amino acid sequenc
34	852	50.9	173	21	AAW84421	Amino acid sequenc
35	852	50.9	187	21	AAW84420	A murine osteoprot
36	842	50.3	173	21	AAW84422	Mouse FLAG-murine
37	830	49.6	170	22	AAU08386	An osteoprotegerin
38	804.5	48.0	188	21	AAW84423	DNA encoding osteo
39	794.5	47.4	182	21	AAW84424	Amino acid sequenc
40	771	46.0	173	21	AAW84425	Mouse OBM protein
41	768	45.9	160	21	AAE08273	Human RANKL. Homo
42	746	44.5	139	21	AAW91023	An osteoprotegerin
43	741	44.2	152	22	AAW67248	Mouse OBM protein
44	732	43.7	173	21	AAW84426	Human RANKL. Homo
45	387	23.1	74	21	AAW91020	Mouse OBM protein

ALIGNMENTS

RESULT 1

AAW83194
ID AAW83194 standard; Protein: 316 AA.

XX AC AAW83194;

XX DT 11-FEB-1999 (first entry)

XX Human osteoprotegerin binding protein from the 32D-F3 ins.

XX Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
XX osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
XX hypercalcaemia; osteoclast differentiation and activation receptor;
XX Paget's disease.

XX OS Homo sapiens.

XX PN WO9846751-A1.

XX PD 22-OCT-1998.

XX PF 15-APR-1998; 98WO-US07584.

XX PR 30-MAR-1998; 98US-0052521.

XX PR 16-APR-1997; 97US-0842842.

XX PR 23-JUN-1997; 97US-0880855.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ;

XX DR WPI; 1998-594578/50.

XX DR N-PSDB; AAV70284.

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 XX
 PS Claim 19; Fig 1; 47pp; English.
 XX
 CC The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OC) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 SQ Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 19; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYKLSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYGYKLSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLDSTLESDTLPDCRRMKQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLDSTLESDTLPDCRRMKQ 120
 QY 121 AFQGAQVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 DB 121 AFQGAQVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 QY 181 VTLSWYHTRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 DB 181 VTLSWYHTRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 QY 241 VKVTSIKIPSSHNLKGGSTKNWGSNEFHFFYSINVGFFKLAGEEISIQVSNPSLLDP 300
 DB 241 VKVTSIKIPSSHNLKGGSTKNWGSNEFHFFYSINVGFFKLAGEEISIQVSNPSLLDP 300
 QY 301 DDQATYFGAFKQVQDID 316
 DB 301 DDQATYFGAFKQVQDID 316
 RESULT 2
 AA#83017
 ID AA#83017 standard; Protein; 316 AA.
 XX
 AC AA#83017;
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
 XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism.
 XX
 OS Unidentified.
 XX

PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 DR WPI; 1998-594563/50.
 DR N-PSDB; AAV69886.
 XX
 PT Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 XX
 PS Claim 8; Pages 106-108; 151pp; Japanese.
 XX
 CC The present sequence represents an osteoclastogenesis inhibitory factor
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 XX
 SQ Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 19; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYGYKLSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
 DB 1 MRRASRDYGYKLSSEMGSGPGVPHGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLDSTLESDTLPDCRRMKQ 120
 DB 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHFNAGLDSTLESDTLPDCRRMKQ 120
 QY 121 AFQGAQVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 DB 121 AFQGAQVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPAPFAHLTINAASIPSGSHK 180
 QY 181 VTLSWYHTRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 DB 181 VTLSWYHTRGWAKISNMTLSNGLKRVNODGFYLLYANICFRHETSGSVPTDYLQMWY 240
 QY 241 VKVTSIKIPSSHNLKGGSTKNWGSNEFHFFYSINVGFFKLAGEEISIQVSNPSLLDP 300
 DB 241 VKVTSIKIPSSHNLKGGSTKNWGSNEFHFFYSINVGFFKLAGEEISIQVSNPSLLDP 300
 QY 301 DDQATYFGAFKQVQDID 316
 DB 301 DDQATYFGAFKQVQDID 316

Query Match 100.0%; Score 1675; DB 20; Length 316;

The present invention describes a genomic DNA encoding a protein having an activity of supporting or promoting differentiation and maturation of osteoclasts. The genomic DNA encoding a protein has the following properties: (a) combines specifically with osteoclastogenesis inhibitory factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw) of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) under a nonreducing condition and the apparent mw when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c) has an activity of supporting or promoting differentiation and maturation of osteoclast in the co-culture of mouse osteoblast-like stroma cell and mouse spleen cell in the presence of a bone absorption promoting factor.

XX PI Halkier T, Haaning J;
 XX WPI: 2000-271444/23.
 DR N-PSDB; AAZ99965.
 DR
 XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -
 XX
 XX Claim 17; Page 81-82; 110pp; English.
 XX
 XX The present sequence represents a murine osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 XX
 XX Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 21; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MRRASRDYKGLRSSEMGSGVPHEGPHLPAPSAPAPAPPAAASRSNMFALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDCRRMQ 120
 Db 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDCRRMQ 120
 QY 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQKPEAQPFAHLTINAAISPGSGHK 180
 Db 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQKPEAQPFAHLTINAAISPGSGHK 180
 QY 181 VTSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMY 240
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 Db 301 DDATYFGAFKVDID 316
 RESULT 7
 ID AAY84419 standard; Protein; 316 AA.
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 XX AC AAY84419;
 XX
 XX 25-JUL-2000 (first entry)
 XX
 XX Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
 DE
 XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
 KW tumour necrosis factor receptor; type II transmembrane protein;
 KW osteoclast differentiation; CSF-1; osteoclast activator;
 KW immune response; osteoporosis; bone resorption.
 XX
 XX Mus musculus.

XX FH Location/Qualifiers
 FT Region 49..69
 FT Domain /note= "transmembrane region"
 FT 70..157
 FT /note= "extracellular stalk domain"
 FT 158..317
 FT /note= "active ligand moiety"
 XX
 XX WO200015807-A1.
 XX
 XX 23-MAR-2000;
 XX
 XX 13-SEP-1999; 99WO-DK00481.
 XX
 XX 15-SEP-1998; 98DK-0001164.
 PR 02-OCT-1998; 98US-0102896.
 XX
 XX (MEBI-) M & E BIOTECH AS.
 XX
 XX Halkier T, Haaning J;
 XX WPI: 2000-271444/23.
 DR N-PSDB; AAZ99966.
 XX
 XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
 PT to treat, prevent and ameliorate osteoporosis -
 XX
 XX Claim 17; Page 85-86; 110pp; English.
 XX
 XX The present sequence represents a murine osteoprotegerin ligand (OPGL).
 CC Osteoprotegerin is a secreted member of the tumour necrosis factor
 CC receptor family, which blocks osteoclastogenesis in a dose dependent
 CC manner. The OPGL protein is synthesised as a type II transmembrane
 CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
 CC is a potent osteoclast differentiation factor when combined with CSF-1.
 CC It is not capable of inducing osteoclast differentiation in the absence
 CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
 CC specification describes a method for the in vivo down-regulation of
 CC OPGL activity in an animal. The method comprises using at least one OPGL
 CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
 CC an immune response in the animal. The method and OPGL polypeptide are
 CC useful for treating, preventing and ameliorating osteoporosis or other
 CC diseases or conditions characterised by excessive bone resorption.
 XX
 XX Sequence 316 AA;
 Query Match 100.0%; Score 1675; DB 21; Length 316;
 Best Local Similarity 100.0%; Pred. No. 2.6e-143;
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRRASRDYKGLRSSEMGSGVPHEGPHLPAPSAPAPAPPAAASRSNMFALLGLGLGQ 60
 Db 1 MRRASRDYKGLRSSEMGSGVPHEGPHLPAPSAPAPAPPAAASRSNMFALLGLGLGQ 60
 QY 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDCRRMQ 120
 Db 61 VVCSIALFLYFRAQMDPNRISEDSHCFYRILRLHENAGLQDSTLESDTLPDCRRMQ 120
 QY 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQKPEAQPFAHLTINAAISPGSGHK 180
 Db 121 AFOGAVQKELQHVGPQFSGAPAMEGSWLDVAQKPEAQPFAHLTINAAISPGSGHK 180
 QY 181 VTSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMY 240
 Db 181 VTSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMY 240
 QY 241 VKTSIKIPSSHNLMKGGSTKNWSGNSSEHFFYSINVGGFFKLAGEEISIQVNSPDLDP 300
 Db 241 VKTSIKIPSSHNLMKGGSTKNWSGNSSEHFFYSINVGGFFKLAGEEISIQVNSPDLDP 300
 QY 301 DDATYFGAFKVDID 316
 Db 301 DDATYFGAFKVDID 316

Db 301 DQDATYFGAFKVDID 316

RESULT 8
AAU78289
ID AAU78289 standard; Protein; 316 AA.

XX
AC AAU78289;
XX
DT 18-JUN-2002 (first entry)
XX
DE Mouse TRANCE protein.
XX
KW Mouse; tumour necrosis factor-related activation induced cytokine;
KW TRANCE; dwarfism; osteopetrosis; craniofacial-skeletal discrepancy;
KW bone damage; cartilage damage; traumatic injury; surgery; osteoarthritis;
KW rheumatoid arthritis; acromegaly; gigantism; exostosis; cartilage;
KW exostosis bursata; multiple osteocartilaginous exostosis; chondrocyte;
KW cartilage growth; skeletal growth.

QS Mus sp.
WO200216551-A2.
XX
PD 28-FEB-2002.
XX
PF 20-AUG-2001; 2001WO-US26101.
XX
PR 18-AUG-2000; 2000US-226197P.
XX
PA (UYWA-) UNIV MASSACHUSETTS MEDICAL CENT.
XX
PI Choi Y, Odgren PR, Marks SC;
XX
DR WPI; 2002-304119/34.
XX
DR N-PSDB; ABK12880.
XX
PT Treating mammal having disorder characterised by abnormal
PT cartilage/skeletal growth such as dwarfism, acromegaly, by
PT administering tumour necrosis factor-related activation induced
PT cytokine-modulating agent to mammal
XX
PS Disclosure; Fig 10; 55pp; English.

CC The present invention relates to a new method of treating a mammal
CC having a disorder comprising insufficient or excessive cartilage or
CC skeletal growth. The method of the invention involves administering to
CC the mammal a tumour necrosis factor-related activation induced cytokine
CC (TRANCE)-modulating agent. The method is useful for treating a mammal
CC having a disorder comprising insufficient or excessive cartilage or
CC skeletal growth, where the disorder comprising insufficient cartilage
CC or skeletal growth is selected from dwarfism, osteopetrosis,
CC craniofacial-skeletal discrepancies and bone or cartilage damage
CC resulting from traumatic injury, surgery, osteoarthritis or rheumatoid
CC arthritis, and disorders comprising excessive cartilage or skeletal
CC growth are selected from acromegaly, gigantism, exostosis, cartilage,
CC exostosis bursata and multiple osteocartilaginous exostoses. The method
CC is useful for inhibiting chondrocyte differentiation. The present
CC amino acid sequence represents the mouse TRANCE protein of the invention.
CC TRANCE is a member of the tumour necrosis factor family and acts
CC directly on cartilage-producing cells (chondrocytes).

XX Sequence 316 AA;
SQ
Query Match 100.0%; Score 1675; DB 23; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.6e-143;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRRASRDYKYLRSSEMGSGVPEGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEMGSGVPEGPHLPAPAPAPPPAASRSMFLALLGLGLGQ 60
Oy 61 VVCSIALFLYFRAQMDPNRISDSTFCFRIILRLHENAGLQDSTLESEDTLPDSRRMQ 120

Db 61 VVCSIALFLYFRAQMDPNRISDSTFCFRIILRLHENAGLQDSTLESEDTLPDSRRMQ 120
Oy 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRGPEAOPFAHLTINAAASIPSGSHK 180
Db 121 AFOGAVOKELQHVGPQRFSGAPAMMEGSLDVAQRGPEAOPFAHLTINAAASIPSGSHK 180
Oy 181 VTLSSWYHHRGWAKISNMTLSNGKLRVNODGFFYYLYANICFRHHETSGSVPTDYQLAVY 240
Db 181 VTLSSWYHHRGWAKISNMTLSNGKLRVNODGFFYYLYANICFRHHETSGSVPTDYQLAVY 240
Oy 241 VVTKTSIKIPSSHNLMKGGSTKNNSGNSEPHFYSINVGPFKLRAGEISIOVSNPSLLDP 300
Db 241 VVTKTSIKIPSSHNLMKGGSTKNNSGNSEPHFYSINVGPFKLRAGEISIOVSNPSLLDP 300
Oy 301 DQDATYFGAFKVDID 316
Db 301 DQDATYFGAFKVDID 316

RESULT 9
AAB82092
ID AAB82092 standard; Protein; 318 AA.
XX
AC AAB82092;
XX
DT 29-JUN-2001 (first entry)
XX
DE Rat osteoclast differentiation factor, ODF.
XX
KW Rat; osteoclast formation inducer; vaccine; gene therapy;
KW Osteoclast Differentiation Factor; bone.
XX
OS Rattus sp.
XX
PN WO200123549-A1.
XX
PD 05-APR-2001.
XX
PF 29-SEP-2000; 2000WO-AU01202.
XX
PR 29-SEP-1999; 99AU-0003147.
XX
PA (UYWA-) UNIV WESTERN AUSTRALIA.
XX
PI Xu J, Zheng M;
XX
DR WPI; 2001-335526/35.
XX
DR N-PSDB; AAF86481.
XX
PT Novel nucleic acid encoding rat osteoclast differentiation factor
PT useful for modulating activity of a cell, e.g., cell proliferation,
PT cell differentiation and cell viability
XX
PS Claim 5; Fig 2; 81pp; English.

CC The present sequence is the protein sequence for rat Osteoclast
CC Differentiation Factor (ODF). ODF is thought to be directly involved in
CC the differentiation of monocytes/macrophages into osteoclasts.
CC Osteoclasts promote dissolution of the bone matrix and solubilisation of
CC bone salts. The ODF coding sequence is useful in gene therapy, and as
CC hybridisation probes or primers. ODF protein is useful for modulating the
CC activity of cells, e.g., cell proliferation, cell differentiation and
CC cell viability, as immunogens to generate anti-rat ODF antibodies, and
CC as vaccines. Anti-rat ODF antibodies are useful in assay methods for
CC quantifying ODF polypeptides.

XX Sequence 318 AA;
SQ
Query Match 95.3%; Score 1597; DB 22; Length 318;
Best Local Similarity 95.0%; Pred. No. 3e-136;
Matches 302; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 MRRASRDYGYKLLSRSEMGSGPGVPHGPHLPAPAPAPAPPPAASRSMFLALGLGLGQ 60
DB 1 MRRANRDYGYKLLSRSEMGSGPGVPHGPHLPAPAPAPAPPPAASRSMFLALGLGLGQ 60
QY 61 VCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 118
DB 61 VCSIALFLYFRAQMDPNRISSESTHCFYRILRLHENAGLQDSTLESDTLEALPDSCRRM 120
QY 119 KQAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQKPEAQPFAHLTINAAIPSGS 178
DB 121 KQAFQAVQKELQHVGPQRFSGAPAMMEGSLDVAQKPEAQPFAHLTINAAIPSGS 180
QY 179 HKVTLSSWYHGRGWAKISNMTLSNGKLRVNDGFFYILYANICFRHHETSGSVPTDYQLQIM 238
DB 181 HKVTLSSWYHGRGWAKISNMTLSNGKLRVNDGFFYILYANICFRHHETSGSVPTDYQLQIM 240
QY 239 VYVYKTSIKIPSSHNLMKGGSTKNWNSGSEHFYSINVGFFKLRAGEEISIQVSNPSSL 298
DB 241 VYVYKTSIKIPSSHNLMKGGSTKNWNSGSEHFYSINVGFFKLRAGEEISIQVSNPSSL 300
QY 299 DPQDQATYFGAFKVQDID 316
DB 301 DPQDQATYFGAFKVQDID 318

RESULT 10
AAW69956
ID AAW69956 standard; Protein: 294 AA.

XX AC AAW69956;
XX 08-OCT-1998 (first entry)
XX NF-kB receptor activator RANK ligand (RANKL).
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX immune response; inflammatory response; toxic shock; sepsis;
XX RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.
XX OS Mus musculus.
XX PN WO9828426-A2.
XX PD 02-JUL-1998.
XX 22-DEC-1997; 97WO-US23775.
XX 14-OCT-1997; 97US-0064671.
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0813509.
XX (IMMV) IMMUNEX CORP.
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX WPI; 1998-377657/32.
XX N-PSDB; AAV41377.

New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells

Claim 27; Pages 55-57; 80pp; English.

This represents a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an

CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug screening.

XX Sequence 294 AA;

Query Match 92.88; Score 1554; DB 19; Length 294;
Best Local Similarity 99.78; Pred. No. 2.1e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGPHLPAPAPAPPPAASRSMFLALGLGLGQVCSIALFLYFRAQMDPNRISE 82
DB 1 GVPHEGPHLPAPAPAPPPAASRSMFLALGLGLGQVCSIALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQAFQAVQKELQHVGPQRFSGA 142
DB 61 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQAFQAVQKELQHVGPQRFSGA 120
QY 143 PAMMEGSLDVAQKPEAQPFAHLTINAAIPSGSHKVTLSWYHGRGWAKISNMTLSN 202
DB 121 PAMMEGSLDVAQKPEAQPFAHLTINAAIPSGSHKVTLSWYHGRGWAKISNMTLSN 180
QY 203 GKLRVNDGFFYILYANICFRHHETSGSVPTDYQLQIMVYVYKTSIKIPSSHNLMKGGSTKN 262
DB 181 GKLRVNDGFFYILYANICFRHHETSGSVPTDYQLQIMVYVYKTSIKIPSSHNLMKGGSTKN 240
QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSSLDPQDQATYFGAFKVQDID 316
DB 241 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSSLDPQDQATYFGAFKVQDID 294

RESULT 11
AAW68292
ID AAW68292 standard; Protein: 294 AA.

XX AC AAW68292;
XX 08-OCT-1998 (first entry)
XX NF-kB receptor activator RANK ligand (RANKL).
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX immune response; inflammatory response; toxic shock; sepsis;
XX RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX OS Mus musculus.

XX PN WO9828424-A2.

XX PD 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX N-PSDB; AAV41371.

XX New isolated receptor activator of necrosis factor-kappa B - useful

PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis
 PS
 PS Example 7; Pages 55-57; 80pp; English.

XX This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumor necrosis factor (TNF) family. Host cells transfected
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 294 AA;

Query Match 92.88; Score 1554; DB 19; Length 294;
 Best Local Similarity 99.78; Pred. No. 2.1e-132;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPAPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 82
 DB 1 GVPHEGLHPAPSAPAPAPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 60
 QY 83 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 142
 DB 61 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 120
 QY 143 PANMEGSLDVAQRGKPEAQPFALHTINAAISIPSGSHKVTLSSTHWDGAKISNMTLSN 202
 DB 121 PANMEGSLDVAQRGKPEAQPFALHTINAAISIPSGSHKVTLSSTHWDGAKISNMTLSN 180
 QY 203 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVVKTSIKIPSSHNLKMGSTKN 262
 DB 181 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVVKTSIKIPSSHNLKMGSTKN 240
 QY 263 WSGNSEFHYISINVGFFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 316
 DB 241 WSGNSEFHYISINVGFFKLRAGEISIQVSNPSLLDDPDQDATYFGAFKVQDID 294

RESULT 12

AAE08737 AAE08737 standard; Protein; 294 AA.

AAE08737;

15-NOV-2001 (first entry)

Murine receptor activator of NF kappaB ligand (RANKL) protein.

XX Murine; receptor activator of nuclear factor kappaB ligand; RANKL; NF;
 KW tumor necrosis factor; TNF; TNF receptor associated factor; TRAF;
 KW immune response; inflammatory response; graft-versus-host reaction;
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX Mus musculus.

XX US6271349-B1.

XX 07-AUG-2001.

XX 17-DEC-1998; 9808-0215649.

XX 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0077181.
 PR 14-OCT-1997; 97US-0064671.
 PR 23-DEC-1996; 96US-0772330.
 PR 07-MAR-1997; 97US-0813509.
 PR 22-DEC-1997; 97US-0996139.

XX (TMV) IMMUNEX CORP.

PA Dougall WC, Galibert L;

PI WPI; 2001-520313/57.

XX N-PSDB; AAD15310.

DR New receptor activator of NF-kappaB (RANK) polypeptides, useful for
 PT regulating immune response, in screening for RANK inhibitors, or as an
 PT adjunct therapy for disease characterized by neoplastic cells that
 PT express RANK

XX Example 15; Column 65-68; 47pp; English.

CC The patent discloses novel receptor activator of nuclear factor (NF)-
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
 CC of the tumor necrosis factor (TNF) receptor superfamily and associates
 CC with TNF receptor associated factor (TRAF) 2 and 3 which are important
 CC in the regulation of immune and inflammatory response. The receptors
 CC are useful for regulating immune response and in screening for inhibitors
 CC of these receptors. The cytoplasmic domain of RANK is used in developing
 CC assays for inhibitors of signal transduction, e.g. for screening the
 CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
 CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
 CC are useful in ameliorating the negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, acute inflammatory
 CC reactions and the effects of bone resorption. RANK acts as an anti-
 CC apoptotic signal and rescue the cells that express RANK from apoptosis.
 CC Soluble forms of the receptor are used in vivo or in vitro based
 CC screening tests for agonists or antagonists of RANK activity, as
 CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit
 CC transduction of a signal via RANK. RANK compositions are used in the
 CC development of both agonistic and antagonistic antibodies, or as an
 CC adjunct therapy for disease characterised by neoplastic cells that
 CC express RANK. Compounds that interfere with RANK/TRAF6 interactions
 CC are useful for modulating the formation of osteoclasts from osteoclast
 CC precursors and for modulating osteoclast function and activities. They
 CC are used as inhibitors of diseases associated with excess bone resorption
 CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
 CC useful for the expression of recombinant proteins, as probes for analysis
 CC of the presence or distribution of RANK transcripts, while the proteins
 CC are useful in preparing kits for the detection of soluble RANK, or
 CC monitor RANK-related activity. The present sequence is RANK ligand
 CC (RANKL) protein from murine.

XX SQ Sequence 294 AA;

Query Match 92.88; Score 1554; DB 22; Length 294;

Best Local Similarity 99.78; Pred. No. 2.1e-132;

Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPAPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 82

DB 1 GVPHEGLHPAPSAPAPAPPAASRSMFLALLGLGLGVGVCSIALFLYFRQMDPNRISE 60

QY 83 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 142

DB 61 DSTHCFYRILRLHENAGLDSTLESDTLPDSCRRMKQAFQAVOKELQHVGPORFSGA 120

QY 143 PANMEGSLDVAQRGKPEAQPFALHTINAAISIPSGSHKVTLSSTHWDGAKISNMTLSN 202

DB 121 PANMEGSLDVAQRGKPEAQPFALHTINAAISIPSGSHKVTLSSTHWDGAKISNMTLSN 180

QY 203 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVVKTSIKIPSSHNLKMGSTKN 262

DB 181 GKLRVNDGFYLYANICFRHETSGSVPTDYQLQMVVVKTSIKIPSSHNLKMGSTKN 240

QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
 DB 241 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 294

RESULT 13

AAE04425
 ID AAE04425 standard; Protein; 294 AA.

XX AC AAE04425;

DT 04-SEP-2001 (first entry)

DE Murine receptor activator of NF- χ 1 B ligand (RANKL) protein.

KW Murine; receptor activator of NF- χ 1 B; RANK; tumour necrosis factor;
 W CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
 X chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.

OS Mus musculus.

PH Key Location/Qualifiers

FT Region 139..294

FT /note="Receptor binding region"

XX US6242213-B1.

XX 05-JUN-2001.

XX 22-DEC-1997; 97US-0995659.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0077181.

XX 14-OCT-1997; 97US-0064671.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM;

XX WPI; 2001-407216/43.

XX N-PSDB; AAD08714.

XX New DNA molecules, useful for producing ligands (which are useful for
 PT regulating immune response and in screening for inhibitors of NF- χ 1 B
 PT receptor activator) of the receptor activator of NF- χ 1 B (RANK)

XX Example 7; Column 59-62; 43pp; English.

XX The present invention relates to receptor activator of NF- χ 1 B (RANK)
 CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
 CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane
 CC proteins respectively. RANK is a member of the tumour necrosis factor
 CC (TNF) superfamily and it closely resembles CD40 in the extracellular
 CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
 CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
 CC The ligands are useful for regulating immune response and in screening
 CC for inhibitors of RANK. The present sequence is murine RANKL protein.

XX Sequence 294 AA;

XX Query Match 92.8%; Score 1554; DB 22; Length 294;

XX Best Local Similarity 99.7%; Pred. No. 2.1e-132;

XX Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPPPAASRSMFTALLGLGLGQVVCSTALFLYFRAQMDPNRISE 82

DB 1 GVPHEGLHPAPSAPAPPPAASRSMFTALLGLGLGQVVCSTALFLYFRAQMDPNRISE 60

QY 83 DSTPHCFVTRLRLHENAGLDSTLESDTLPSDCRRMKQAFQAVQKELQHVGPQFSGA 142

DB 61 DSTPHCFVTRLRLHENAGLDSTLESDTLPSDCRRMKQAFQAVQKELQHVGPQFSGA 120

QY 143 PAMMEGSLDVAORCKPEAQPFAHLTINAASIPSGSHKVTLSLSSWYHDRGWAKISNMTLSN 202
 DB 121 PAMMEGSLDVAORCKPEAQPFAHLTINAASIPSGSHKVTLSLSSWYHDRGWAKISNMTLSN 180
 QY 203 GKLRYNQDGFYLYANICFRHHETSGSVPTDYQLQLMVYVVKTSIKIPSSHNLKMGSGTKN 262
 DB 181 GKLRYNQDGFYLYANICFRHHETSGSVPTDYQLQLMVYVVKTSIKIPSSHNLKMGSGTKN 240
 QY 263 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 316
 DB 241 WSGNSEHFYSINVGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVDID 294

RESULT 14

AAE01992
 ID AAE01992 standard; Protein; 294 AA.

XX AC AAE01992;

DT 31-JUL-2001 (first entry)

DE Murine RANKL (receptor activator of NF- χ 1 B ligand) protein.

KW Mouse; receptor activator of NF- χ 1 B; RANK; nuclear factor- χ 1 B;
 KW NF- χ 1 B; tumour necrosis factor; TNF; type 1 transmembrane protein;
 KW TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopontin;
 KW inflammatory reaction; bone resorption; gene therapy; immunomodulator;
 KW immune system dysfunction; familial expansile osteolysis; FEO;
 KW early onset Paget's disease of bone; BP; cytostatic.

OS Mus musculus.

XX WO2001136637-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-US31459.

XX 17-NOV-1999; 99US-0442029.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Hughes AE;

XX WPI; 2001-329222/34.

XX N-PSDB; AAD05903.

XX New DNA encoding a receptor activator of NF- χ 1 B polypeptide for the
 PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
 PT Disclosure; Page 74-75; 96pp; English.

XX The present invention relates to a novel receptor, referred to as RANK

XX (receptor activator of NF (nuclear factor)- χ 1 B), a member of TNF
 CC (tumour necrosis factor) receptor superfamily. RANK is a Type I
 CC transmembrane protein that interacts with TNF receptor-associated
 CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
 CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
 CC of the transcription factor NF- χ 1 B, a ubiquitous transcription factor
 CC that is most extensively utilised in cells of the immune system.

XX Inhibition of NF- χ 1 B by RANK antagonists is useful in ameliorating
 CC negative effects of inflammatory reactions, and the effects of excess
 CC bone resorption. The RANK DNAs, proteins and their analogues are useful
 CC for the preparation of pharmaceutical compositions, for infecting target
 CC cells for use in gene therapy applications in diagnosing diseases
 CC associated with RANK, and as targets for use in screening assays. They
 CC may be used in the treatment or diagnosis of immune system dysfunction.
 CC The present invention also encompasses gene therapy methods to correct
 CC gene-activating mutations, associated with e.g. familial expansile
 CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
 CC present amino acid sequence is murine RANKL (murRANKL) protein.

XX Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 22; Length 294;
Best Local Similarity 99.7%; Pred. No. 2.1e-132;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GYPHEGLPAPSAAPAPPPAASRSMFLALGLGQVVCSTALFLYFRAQMDPNRISE 82
DB 1 GYPHEGLPAPSAAPAPPPAASRSMFLALGLGQVVCSTALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQAFQVQKELQHVQPFQFSGA 142
DB 61 DSTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQAFQVQKELQHVQPFQFSGA 120
QY 143 PAMGSGWLDVAQKPEAPQFAHLTINAASIPSGSHKVTLSWYHRCGWAKISNMTLSN 202
DB 121 PAMGSGWLDVAQKPEAPQFAHLTINAASIPSGSHKVTLSWYHRCGWAKISNMTLSN 180
QY 203 GKLRVNDGFFYLXANICFRHETSGVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
DB 181 GKLRVNDGFFYLXANICFRHETSGVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240
263 WSGNSEFHYSINVGSGFFKLRAGEEISIQVSNPDLDPQDQATYFGAFKVDID 316
241 WSGNSEFHYSINVGSGFFKLRAGEEISIQVSNPDLDPQDQATYFGAFKVDID 294

RESULT 15
AAW83195
ID AAW83195 standard; Protein; 317 AA.
AC AAW83195;
XX 11-FEB-1999 (first entry)
XX Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
XX Human: osteoprotegerin binding protein; OPG binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
XX Paget's disease.
XX Homo sapiens.
XX WO9846751-A1.
XX 22-OCT-1998.
XX 15-APR-1998; 98WO-0507584.
XX 30-MAR-1998; 98US-0052521.
XX 16-APR-1997; 97US-0842842.
XX 23-JUN-1997; 97US-0880855.
XX (AMGE-) AMGEN INC.
XX Boyle WJ;
XX WPI; 1998-594578/50.
XX N-PSDB; AAV70285.
XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX Claim 19; Fig 4; 47pp; English.
XX The present sequence is human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OPG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for

detection of OPG binding protein) and to identify compounds that
modulate binding of OPG binding protein to osteoclast differentiation
and activation receptor (ODAR). The nucleic acid molecule encoding OPG
binding protein can be used to detect OPG binding protein-encoding OPG
sequences, e.g. screening for related sequences, also to produce
transgenic animal models, while complementary sequences are used for
antisense regulation of OPG binding protein expression. Modulators of
OPG binding protein, particularly soluble forms of OPG binding protein
or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
disease, periodontal disease, osteoporosis, loosening of prostheses,
optionally in combination with agents that promote bone growth.

XX Sequence 317 AA;
SQ

Query Match 84.6%; Score 1417.5; DB 19; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.4e-120;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYKYLRSSSEMGSGVPGVHGPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 60
DB 1 MRRASRDYKYLRSSSEMGSGVPGVHGPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 59
QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 118
DB 60 VVCSIALFLYFRAQMDPNRISESTHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 119
QY 119 KQAFQAVQKELQHVQKPEAPQFAHLTINAASIPSGSHKVTLSWYHRCGWAKISNMTLSN 178
DB 120 KQAFQAVQKELQHVQKPEAPQFAHLTINAASIPSGSHKVTLSWYHRCGWAKISNMTLSN 179
QY 179 HKVTLSSWYHRCGWAKISNMTLSNGLKRVNDGFFYLXANICFRHETSGVPTDYLQLM 238
DB 180 HKVTLSSWYHRCGWAKISNMTLSNGLKRVNDGFFYLXANICFRHETSGVPTDYLQLM 239
QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHYSIQVSNPDLDPQDQATYFGAFKVDID 298
DB 240 VYVTKTSIKIPSSHNLMKGGSTKNWGSNFEHYSIQVSNPDLDPQDQATYFGAFKVDID 299
QY 299 DPQDQATYFGAFKVDID 316
DB 300 DPQDQATYFGAFKVDID 317

Search completed: April 16, 2003, 12:18:36
Job time : 34.5 secs

A;Accession: A49266

```

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <RND>
A:Cross-references: GB:003470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C:Keywords: glycoprotein; transmembrane protein

Query Match          10.98; Score 183; DB 2; Length 278;
Best Local Similarity 23.48; Pred. No. 9.5e-08;
Matches 75; Conservative 42; Mismatches 107; Indels 96; Gaps 13;

QY 14 SSEMGSG-----PCVPHEGPHLPAPSAPAPP-----PAASRSMFLALL 54
   ||      ||      ||      ||      ||      ||      ||      ||
Db 34 SSGPRGQQRPPPPPPPSPL-PPSPQPPPLPLPLKKNKDNIELWLPVFVEMVLVALV 92

QY 55 GLGLGVVCSIALFLYFRAQMDPNRISDSHTCFYRIILRHENAGLODSTLESEDTLPDS 114
   |||||      |||||      |||||      |||||      |||||      |||||
Db 93 GMGLG-----MYQLPHLOKELAELEAELREFTNH-----SLRVSSPEKQIANEPT 133

QY 115 CRRMKAQFOGAVQKELQHVGPQRFSGAPAMMEGSLDVAQKGPEAPFAHLTN--AA 172
      |      |      |      |      |      |      |      |      |
Db 134 PSETK-----NPRS--VAHLTCNPRSR 153

QY 173 SIPSGSHKVTLSWYHQRGNAKISNMTLSNGLRVNQDGYIYLANICFRHETSGSVPT 232
   |||      |||      |||      |||      |||      |||      |||
Db 154 SIP-----LEWEDTYGTALISGVYKRGGLVINEAGLYFVYSKVYFR-GQSCNSOP- 203

QY 233 DYLLQWTVVKTSTIKPSSHNLKGGGSKNKGSGNEPHTSYINWGGFFKLRAGEBISIQV 292
   |||      |||      |||      |||      |||      |||      |||
Db 204 --LSHKVTM--RNFKYPGDLVIME-EKKLNTCTTQIWAHSSYIGAVENLTVADHLVNI 258

QY 293 SNPSLLDPDQDATYTGAFKV 312
   |||      |||      |||      |||      |||      |||
Db 259 SOLSLINFEESKSTFFGLYKL 278

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```

RESULT 3
A53062
Fas ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53062
R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nagai, Y.
Cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in Fas ligand
A:Reference number: A53062; MUID:94185175; PMID:7511063
A:Accession: A53062
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-279 <TAK>
A:Cross-references: GB:U06948; NID:g473564; PIDN:AAAI7800.1; PID:g473565

Query Match 10.9%; Score 182; DB 2; Length 279;
Best Local Similarity 22.7%; Pred. No. 1.2e-07;
Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;

QY 13 RSSEMGSGVCPVHEGPLHPAPSNAPAPP-----PAASRSMFLALLIGL 57
Db 38 RGPDRRRPPPPPPVPSPL-PPPSQPLPLPLPLKXKDHNTLWLPPVFFMVLVALVGMG 96
QY 58 LGQVVCISALFLVFRAGMDPNRISDSTHCFYRILRLHENAGLDQSTLESDTLPSCCR 117
Db 97 LG-----MYQLFLQKE---LAE-----LREFTNQSLKVSSEKQIANPST--- 134
QY 118 MKQAFQAVOKELQHIYGPVGRSCAPAMMEGSLWDVAQRGKPEAQPFALHTLN--AASIP 175
Db 135 -----PSE-----KKEPRSAHLTGPHRSRIP 157
QY 176 SGSHKVTLSNWHDRGWAKISNMTLSNKLRLVNDQGYILYANICFRHHETSGSVPTDYL 235
Db 158 -----LEWEDTYGALISGVKVKKGGLVINETGLTFYVYSKVYFR-GQSCNNQPLNH- 207
QY 236 QLMYTVVKTSTIKIPSSINLMKGGSTKNWNSSEFHTYSINVGFFFLKLRAGEETISQVSNP 295
Db 236 QLMYTVVKTSTIKIPSSINLMKGGSTKNWNSSEFHTYSINVGFFFLKLRAGEETISQVSNP 295

```

[illegible]

Gene 107, 319-321, 1991
A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor
A:Reference number: JQ1344; MUID:92084125; PMID:1748301

[illegible]

submitted to the EMBL Data Library, September 1991

A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.

A:Reference number: S22052

A:Accession: S22052

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <SAN>

A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.6%; Score 143.5; DB 1; Length 233;
Best Local Similarity 25.6%; Pred. No. 0.00015;
Matches 50; Conservative 36; Mismatches 70; Indels 39; Gaps 11;

Qy 133 IVGPOR--FSGAPAMMGSLDVAQRGK---PEAQFPAHLTINAASIPSGSHKVTLSWY 187

Db 55 VIGPQREFPDPSLI--SPLAQVRSRSPDKPVAVVAN-----PQAEQL---QWL 105

Qy 188 HDRGWAKISN-WTLSNGKLRVNDQGYLYLANICFRHETSGSVPTDYLQL-----M 238

Db 106 NRRANALLANGVELRDNLVWPSEGLYLYSQVLEK-----GQCPSVHLLTHTISRIA 161

Qy 239 VTVVK-----TSIKIPSSHNLKMGSTKNGNSGFHYSINVGPFKLRAGEISIQVSN 294

Db 162 SYQTKVNLLSAIKSCQRETPEGAEPW-----YEPIYLGGVFQLEKGRDLSAE 214

Qy 295 PSLLD-PDQDATYFG 308

Db 215 PDYLDFAESGQVYFG 229

RESULT 10

JH0529

tumor necrosis factor alpha precursor - sheep

A:Alternate names: cachectin; TNF alpha

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: JH0529; S48118; S13114; S20661

R:Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with

A:Reference number: JH0529; MUID:92112044; PMID:1765267

A:Accession: JH0529

A:Molecule type: mRNA

A:Residues: 1-234 <GRE>

A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A:Experimental source: alveolar macrophage

R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A:Reference number: S48118; MUID:92155784; PMID:1786996

A:Accession: S48118

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <NAS>

A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A:Reference number: S13114; MUID:91067496; PMID:2251151

A:Accession: S13114

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOD>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is probably

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; F:1-77/Domain: propeptide #status predicted <PRO>

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;
Best Local Similarity 25.8%; Pred. No. 0.00024;
Matches 51; Conservative 31; Mismatches 72; Indels 44; Gaps 11;

Qy 133 IVGPQFSGAPAMMGSLDVAQRGKPEAQFPAHLTINAASIPSG---SHKVTLSWYH 188

Db 55 VIGPQREFGSPA-----GPSFNRPLVQ-VLRSSQASNNKPVAVVANISAPG 101

Qy 189 DRGWA-KISNWTLSNG-KLRVNDQ---DGFTYLYLANICFRHH-----ETSGSVP 231

Db 102 QLRWGDVSANALMANGVELKDQLVVPDGLYLYISQVLEFRGHGCPSTPLFLTHTISRIA 161

Qy 232 TDYQLQMVTVKTSIKIPSSHNLKMGSTKNGNSGFHYSINVGPFKLRAGEISIQ 291

Db 162 VSY-QTKVNL-SAIKSPCHRETLEGAEPW-----YEPIYQGVFQLEKGRDLSAE 212

Qy 292 VSNPSLLD-PDQDATYFG 308

Db 213 INLPEYLDFAESGQVYFG 230

RESULT 11

S11688

tumor necrosis factor alpha precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000

C:Accession: S11688

R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.

Nucleic Acids Res. 18, 5563, 1990

A:Title: Gene sequence of feline tumor necrosis factor alpha.

A:Reference number: S11688; MUID:91016860; PMID:2216740

A:Accession: S11688

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-233 <MCG>

A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777

C:Genetics:

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:19/20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.4%; Score 140; DB 2; Length 233;
Best Local Similarity 25.1%; Pred. No. 0.00029;
Matches 50; Conservative 35; Mismatches 74; Indels 40; Gaps 10;

Qy 124 GAVQKELQHVGPQFSGAPAMMGSLDVAQRGKPEAQFPAHLTINAASIPSGSHKVTL 183

Db 57 GPQREELPH--GLQLINPLPOTLRSS-----SRTPSDKPVAVVAN---PEAEGQLQR 104

Qy 184 SSWYHGRGAKISN-WTLSNGKLRVNDQGYLYLANICFRHETSGSVPTDYLQL----- 237

Db 105 LS---RRANALLANGVELTDNLKVPDGLYLYISQVLEF---TGQCPSTHVLTTAHS 157

Qy 238 ---WTVVK---TSIKIPSSHNLKMGSTKNGNSGFHYSINVGPFKLRAGEISIQ 290

Db 158 RFAVSTQTKVNLNLSAIKSPQRETPEGAEPW-----YEPIYLGGVFQLEKGRDLS 210

Qy 291 QVSNPSLLD-PDQDATYFG 308

Db 211 EINLPAYLDFAESGQVYFG 229

Query Match 8.18; Score 135.5; DB 2; Length 235;

Search completed: April 16, 2003, 12:20:42
Job time : 15.5 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:16:16 ; Search time 9.5 Seconds
(without alignments)

1379.634 Million cell updates/sec

Title: US-09-787-126-6

Perfect score: 1675

Sequence:

1 MRRASRDYGYKLSSEPMG.....LLDPDQDATYGFAPKVQDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	1 TN11_MOUSE	O35235 m tumor nec
2	1597	95.3	318	1 TN11_MOUSE	O95e2 x tumor nec
3	1417.5	84.6	317	1 TN11_HUMAN	O14788 h tumor nec
4	258.5	15.4	281	1 TN10_HUMAN	P50591 homo sapien
5	244	14.6	291	1 TN10_MOUSE	P50592 mus musculus
6	188.5	11.3	261	1 TNF5_CALJA	Q9bdn3 callithrix
7	185.5	11.1	261	1 TNF5_BOVIN	P51749 bos taurus
8	183	10.9	278	1 TNF6_RAT	P36940 rattus norv
9	182.5	10.9	261	1 TNF5_AOTTR	Q9bdm3 aotus trivi
10	182	10.9	279	1 TNF6_MOUSE	P41047 mus musculus
11	179.5	10.7	282	1 TNF6_PIG	Q9bea8 sus scrofa
12	178	10.6	280	1 TNF6_MACMU	Q9myl6 macaca mula
13	177	10.6	280	1 TNF6_CERTO	Q9bdn1 cercocebus
14	176.5	10.5	261	1 TNF5_MACMU	Q9bdc7 macaca mula
15	173.5	10.4	281	1 TNF6_HUMAN	P48023 homo sapien
16	171.5	10.2	261	1 TNF5_HUMAN	P29965 homo sapien
17	168.5	10.1	272	1 TNF5_CHICK	Q918d8 gallus gall
18	164	9.8	260	1 TNF5_FELCA	O97605 felis silve
19	159.5	9.5	261	1 TNF5_PIG	Q95mq5 sus scrofa
20	157	9.4	234	1 TNFA_CAVPO	P51435 cavia porce
21	157	9.4	260	1 TNF5_MOUSE	P27548 mus musculus
22	154	9.2	260	1 TNF5_CANFA	O97626 canis fami
23	151	9.0	240	1 TNF5_MACNE	Q9bdm7 macaca neme
24	149	8.9	234	1 TNFA_HORSE	P29553 equus cabal
25	148.5	8.9	233	1 TNFA_MACFA	P79337 macaca fasc
26	147.5	8.8	233	1 TNFA_MACMU	P48094 macaca mula
27	147.5	8.8	310	1 TNFC_MARMO	Q9jmi0 marmota mon
28	146.5	8.7	235	1 TNFA_MOUSE	P06804 mus musculus
29	146.5	8.7	239	1 TN14_MOUSE	Q9qyh9 mus musculus
30	145	8.7	260	1 TNF5_RAT	O9z2v2 rattus norv
31	143.5	8.6	233	1 TNFA_PAPHU	O77510 papio hamad
32	143.5	8.6	233	1 TNFA_PAPSP	P33620 papio sp. (
33	141	8.4	234	1 TNFA_SHEEP	P23383 ovis aries

RESULT 1

TN11_MOUSE

ID	TN11_MOUSE	1	STANDARD;	PRT;	316 AA.
AC	O35235; O35306; Q9RIY0; Q9JJK8; Q9JJK9;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor, ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor) (OCIF).				
GN	TNFSF11 OR RANKL OR TRANCE OR OPGL.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Hybridoma;				
RX	MEDLINE=97460112; PubMed=9312132;				
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;				
RA	"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells."				
RT	J. Biol. Chem. 272:25190-25194 (1997).				
RL	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Thymic lymphoma;				
RX	MEDLINE=98032977; PubMed=9367155;				
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;				
RA	"A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."				
RL	Nature 390:175-179 (1997).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=98227661; PubMed=9568710;				
RA	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;				
RA	"Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."				
RL	Cell 93:165-176 (1998).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	TISSUE=Bone marrow stroma;				
RX	MEDLINE=98188248; PubMed=9520411;				
RA	Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M., Mochizuki S.-I., Tomoyasu A., Yan K., Goto M., Murakami A., Tsuda E., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;				

O95150 homo sapien
P9101 felis silve
P51742 canis fami
P01375 homo sapien
P13296 capra hircu
P04924 oryctolagus
P36939 peromyscus
Q03557 homo sapien
Q06599 bos taurus
P23563 sus scrofa
O35734 marmota mon
P16599 rattus norv

ALIGNMENTS

DR	EMBL; AF013171; AAC51762.1; -.
DR	EMBL; AB037599; BAA90488.1; -.
DR	HSSP; P50591; 1DOG.
DR	Genew; HGNC:11926; TNFSF11.
DR	MIM; 602642; -.
DR	InterPro; IPR003636; TNE_abc.
DR	InterPro; IPR000478; TNE_family.
DR	Pfam; PF00229; TNE; 1.
DR	ProDom; PD002012; TNE_abc; 1.
DR	SMART; SM00207; TNE; 1.
DR	PROSITE; PSQ0251; TNE_1; FALSE_NEG.
DR	PROSITE; PS50049; TNE_2; 1.
KW	Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW	Signal-anchor; Alternative splicing.
FT	CHAIN 1 317
FT	CHAIN 140 317
FT	DOMAIN 1 47
FT	TRANSMEM 48 58
FT	DOMAIN 69 317
FT	SITE 139 140
FT	CARBOHYD 171 171
FT	CARBOHYD 198 198
FT	VARSPLIC 1 47
FT	VARSPLIC 1 73
FT	CONFLICT 194 194 A -> G (IN REF. 4).
FT	SEQUENCE 317 AA; 35478 MW; 766176446348097F CRC64;
FT	SEQ
Query Match	84.6%; Score 1417.5; DB 1; Length 317;
Best Local Similarity	84.3%; Pred. No. 5e-110;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;	
QY	1 MRASRDYGYKLRSSEMGSGPGVHPHEGLHAPSAPAPAPPAAASRMFLALGLGLQG 60
DB	1 MRASRDYTYLKGSEMGGGPGAPHEGPLH-APPPPHAPQHPAASRMFVALGLGLQG 59
QY	61 VCSIALFYFRAQMPNRISESTHCFYRILRLHENAGLDSTLESED--LPDSCRM 118
DB	60 VCVSVALFFYFRAQMPNRISEDTHCIIYLRLHENADFQDTLESQDTKLIIPDCRR 119
QY	119 KOAFQAVOKELQHIVGPQRFGAPAMEGSWLDVAQRKPFAOPFAHLTINAASIPGS 178
DB	120 KOAFQAVOKELQHIVGSHIRAEKAEMVDGSLDLAKRKLEAQPFPAHLTNATIDPSGS 179
QY	179 HKYTLSWSYHDRCGWAKISNTLSNGKLVRNODGFYIYANICFRHHETSGVPDYQLQM 238
DB	180 HRYLSWSYHDRCGWAKISNTMFSNGKLIVNODGFYIYANICFRHHETSGDLAYEYLQLM 239
QY	239 VYVKTSIKIPSSHNLKMGGSTKNWSCNSEFHYSINVGGFFFKLRAGEEISIQVSNPSLL 298
DB	240 VYVKTSIKIPSSHNLKMGGSTKYWSCNSEFHYSINVGGFFFKLRSGEEISIEVSNPSLL 299
QY	299 DPQDATYGAFCRVQIID 316
DB	300 DPQDATYGAFCRVYRID 317
RESULT 4	
TN10_HUMAN	
ID	TN10_HUMAN STANDARD; PRT; 281 AA.
AC	P50591;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related
DE	apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).
GN	TNFSF10 OR TRAIL OR APO2L.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI TaxId=9606;

RN P
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 family that induces apoptosis.";
 RL Immunology 3:673-682(1995).
 (2)
 RN P
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-96278649; PubMed-8663110;
 RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,
 RA Ashkenazi A.;
 RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
 necrosis factor cytokine family.";
 RL J. Biol. Chem. 271:12687-12690(1996).
 (3)
 RN P
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 RX MEDLINE-20017054; PubMed-10549288;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 (4)
 RN P
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RX PubMed-10542098;
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.;
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 (5)
 RN P
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RX MEDLINE-99413670; PubMed-10485660;
 RA Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.;
 RT "2.8 A resolution crystal structure of human TRAIL, a cytokine with
 selective antitumor activity.";
 RL Immunify 11:253-261(1999).
 (6)
 RN P
 RP FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 possibly also to TNFRSF10E/OPG. Induces apoptosis. Its activity
 may be modulated by binding to the decoy receptors
 TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF10E/OPG that cannot
 induce apoptosis.
 (7)
 RN P
 RP COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 trimer.
 (8)
 RN P
 RP SUBUNIT: Homotrimer.
 (9)
 RN P
 RP SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 (10)
 RN P
 RP TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 AND PROSTATE
 (11)
 RN P
 RP SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 (12)
 RN P
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 or send an email to license@isb-sib.ch).
 (13)
 RN P
 RP EMBL: U37518; AAC50332.1;
 RN P
 RP EMBL: U57059; AAB01233.1;
 RN P
 RP Genbank: HGNC:11925; TNFSF10.
 RN P
 RP MIM: 603598;
 RN P
 RP PDB: 1D0G; 22-OCT-99.
 RN P
 RP PDB: 1D4V; 01-NOV-99.
 RN P
 RP PDB: 1D2Q; 11-FEB-00.
 RN P
 RP InterPro: IPR003636; TNF_abc.
 RN P
 RP InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF: 1.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF: 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS00449; TNF_2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 ZINC: 3D-structure.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
 FT METAL 230 230 ZINC.
 FT SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;
 SQ SEQUENCE 281 AA; 32509 MW; DDAAF78DAAB2F6D CRC64;
 Query Match 15.4%; Score 258.5; DB 1; Length 281;
 Best Local Similarity 26.4%; Pred. No. 3e-14;
 Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
 QY 43 PAASRSMELALGLGQVVCSSIALFLYFRAQMD--PNRISDSTHCFYRLRLHENAGL 100
 DB 10 PSLGTCVLIVITVLLSLCVAVTYVFTNELKQMDKYSGIACF-----LKEDDSY 64
 QY 101 QDSTLESDTLPSDCRRMKQAFQGVOK-----ELQHVGPQRFSGAPAMM 146
 DB 65 WDP--NDESMNSPCVQVWQVLRQLVRLMILRTSETISTVQEKQNISPL----- 113
 QY 147 EGSWLDVAORGPFAHPT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
 DB 114 -----VREGRQVRA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSHSFLS 165
 QY 197 NMTLSNGKLRVNDGFYLYANICPRHETSGSPVDYQLQLVVYVVKTSKIPSSHNLMK 256
 DB 166 NLHLRNGELVHKEGFIYIYQTFYFQBEIKENTKNDKQVQYIYKYT-SYDPILLMK 224
 QY 257 CGSTKNKNSGFHFYSINWGGFFKLAGEEISIQVSNPDLDPDQDAYFAGKV 312
 DB 225 SARNSCWSKDAEGLYSIYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAFV 280
 RESULT 5
 ID TN10_MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96111955; PubMed-8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.;
 RT "Identification and characterization of a new member of the TNF
 family that induces apoptosis.";
 RL Immunology 3:673-682(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 possibly also to TNFRSF10E/OPG. Induces apoptosis. Its activity
 may be modulated by binding to the decoy receptors
 TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF10E/OPG that cannot
 induce apoptosis.
 CC -1- SUBUNIT: HOMOTRIMER (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

DD LUKAANTH--SSAKPCQCSHNLGGIFELQPGASVFNVIDPQSQVSHGTGTFISGGLKL 401

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RESULT 7
TNF5_BOVIN
ID TNF5_BOVIN STANDARD; PRT; 261 AA.
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (TNF-
DE related activation protein) (TRAP) (T cell antigen GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
C TISSUE=Blood;
RX MEDLINE=96006582; PubMed=7590981;
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
RL Immunogenetics 42:430-431(1995).
CC -!- FUNCTION: Cytokine that binds to TNFSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IgE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
DR EMBL; 248469; CAA88363.1; -
DR HSSP; P29965; ITALY.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
DR CHAIN 1 261
DR CHAIN 113 261
DR CHAIN 261
DR DOMAIN 1 22
DR TRANSMEM 23 46
DR DOMAIN 47 261
DR SITE 112 113
DR DISULFID 178 218
DR CARBOHYD 240 240
DR SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;
Query Match 11.1%; Score 185.5; DB 1; Length 261;
Best Local Similarity 25.1%; Pred. No. 3e-08;
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;
QY 32 PAPSAPAPAPPAASRSMFLALIGLIGLQGVCSIALF-LYFRAQMDPNRISDSTHCFTYR 90

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RESULT 8
TNF6_RAT
ID TNF6_RAT STANDARD; PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
DE ligand).
GN TNFSF6 OR FASL OR APTLGL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94084792; PubMed=7505205;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family."
RL Cell 75:1169-1178(1993).
CC -!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
CC transduces the apoptotic signal into cells. May be involved in
CC cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
CC peripheral tolerance, in the antigen-stimulated suicide of mature
CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
CC modulates its effects (By similarity).
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
CC similarity).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U03470; AAC52129.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_abc; 1.

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DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN TNFSF6 OR FASL OR APTL1G1 OR GLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RP MEDLINE=94185175; PubMed=7511063;
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
 RA Suda T., Nagata S.
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 RT mutation in the Fas ligand."
 RL Cell 76:969-976(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
 RP STRAIN=C57BL/6;
 RX MEDLINE=95388076; PubMed=7544870;
 RA Peitsch M.J., Tschoep J.J.
 RT "Comparative molecular modelling of the Fas-ligand and other members
 RT of the TNF family."
 RL Mol. Immunol. 32:761-772(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RP MEDLINE=95196085; PubMed=7889405;
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
 RT TNF family gene cluster."
 RL Immunity 1:131-136(1994).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RP STRAIN=BALB/c;
 RA Fenner M.H., Shioda T., Isselbacher K.J.;
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
 RT two amino acids."
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RP STRAIN=C3H; TISSUE=Spleen;
 RX MEDLINE=20021694; PubMed=10552956;
 RA Ayrolidi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,
 RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
 RT "Cloning and expression of a short Fas ligand: A new alternatively
 RT spliced product of the mouse Fas ligand gene."
 RL Blood 94:3456-3467(1999).
 RN [6]
 RP CHARACTERIZATION OF VARIANT GLD.
 RX MEDLINE=96091792; PubMed=7495745;
 RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,
 RA Rousseau M., Bron C., Renno T., French L., Tschoep J.;
 RT "Characterization of the non-functional Fas ligand of gld mice."
 RL Int. Immunol. 7:1381-1386(1995).
 RN [7]
 RP VARIANT'S ALA-184 AND GLY-218.
 RP STRAIN=Various;
 RX PubMed=9108079;
 RA Kayagaki N., Yamaguchi N., Nagao F., Matsuo S., Maeda H., Okumura K.,
 RA Yagita H.;
 RT "Polymorphism of murine Fas ligand that affects the biological
 RT activity."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3914-3919(1997).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
 CC modulates its effects (By similarity).

CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
 CC Secreted (isoforms FASL and FASLS).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
 CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
 CC INTERACTION.
 CC -1- PFM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
 CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
 CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC EMBL; U06948; AAA17800.1;
 CC EMBL; U10984; AAA19778.1;
 CC EMBL; S78752; AAB33780.1;
 CC EMBL; U58995; AAB02915.1;
 CC EMBL; AF119335; AAD52106.1;
 CC HSSP; P01375; 4TSV.
 CC MGD; MGI:99255; Tnfsf6.
 CC InterPro; IPR003636; TNF_abc.
 CC InterPro; IPR000478; TNF_family.
 CC Pfam; PF00229; TNF; 1.
 CC ProDom; PD002012; TNF_abc; 1.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; 1.
 CC PROSITE; PS50049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
 KW Disease mutation; Polymorphism; Tumor necrosis factor ligand superfamily
 KW MEMBER 6, MEMBRANE FORM.
 FT CHAIN 1 279
 FT CHAIN 128 279
 FT DOMAIN 1 78
 FT TRANSMEM 79 100
 FT DOMAIN 101 279
 FT DOMAIN 4 69
 FT DOMAIN 45 51
 FT SITE 127 128
 FT DISULFID 200 231
 FT CARBOHYD 117 117
 FT CARBOHYD 182 182
 FT CARBOHYD 248 248
 FT CARBOHYD 258 258
 FT VASPLIC 1 210
 FT VARIANT 184 184
 FT VARIANT 218 218
 FT VARIANT 273 273
 FT SEQUENCE 279 AA; 31442 MW; 37972E2726E0A1CA CRC64;
 SQ

Query Match 10.9%; Score 182; DB 1; Length 279;
 Best Local Similarity 22.7%; Pred. No. 6.3e-08;
 Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;
 QY 13 RSSEMGSGGVPHGPHLPAPSAPAPP-----PAAGRSMFLALLGLG 57
 Db 38 RGPQRRPPPPPPVSP-PPPSQPLPLPLPLKKKDHNTNLWLPLVFFVFLVALVGMG 96
 QY 58 LGQVCSIALFLYFRQMDPNRISESTGCFYRILRLHFNAGLQDSTLSEDTLPSCRR 117

proteolytic processing (By similarity).

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; AB027297; BAB40919.1; -
EMBL; AY033634; AAK56449.1; -
EMBL; AF397407; AAB84408.1; -
EMBL; AB069764; BAB64291.1; -
HSP; P01375; 4TSV.
InterPro: IPR003636; TNF abc.
InterPro: IPR000478; TNF_family.
Pfam: PF00229; TNF; 1.
PRINTS; PD001234; TNCR0SISFCT.
ProDom; PD002012; TNF abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
CHAIN 1 282
FT FT CHAIN 131 282
FT FT CHAIN 131 282
FT FT DOMAIN 1 82
FT FT TRANSMEM 83 103
FT FT DOMAIN 104 282
FT FT DOMAIN 4 70
FT FT DOMAIN 45 56
FT FT SITE 130 131
FT FT DISULFD 203 234
FT FT CARBOHYD 185 195
FT FT CARBOHYD 251 251
FT FT CARBOHYD 261 261
FT FT CONFLICT 5 5
FT FT CONFLICT 57 57
FT FT SEQUENCE 282 AA; 31756 MW; 6743DAI145671FB CRC64;
Query Match 10.7%; Score 179.5; DB 1; Length 282;
Best Local Similarity 21.6%; Pred. No. 1e-07;
Matches 70; Conservative 42; Mismatches 105; Indels 107; Gaps 10;
QY 20 SGPGVEGPHLPAPSAAPPAPASRS-----MF 50
DB 35 SVFGRP-GRRPPPPPPPPPPPTLLPSPLPPPLPKKRDHNAGLCLLVMFMVL 92
QY 51 LALLGLGVQCVCIALFLFYRAOMPNRISEDTHCFYRLRHENGLQDSLESDT 110
DB 93 VALVGLGLG----MFOFLHLOKE-----LTRELRESASGRHT-- 124
QY 111 LPDCSRMRKQAOFAGVKELQHIVTGPFQSFAPAMMEGSMLDVAQRGKPAPFAHLT-- 168
DB 125 -----ESSLEKQIGHNPLNSE-----KKELRVAHLTGK 153
QY 169 INAAIPSGSHKYTLSSWYHDRGWAKISNNMTLSNGKLVRNQDGYLYLANICFRHHETSG 228
DB 154 PNSRSIP-----LEWEDTYGIALVSGVKYMGKSLVINDTGLIFYSKVIYRGGYCINN 205
QY 229 SVPTDIQLMVYVVKYSIKIPSSHNLKMGSTNWNSGNSEFHYSINVGFFKLAGEEI 288
DB 206 Q-----PLSHKVYITRNRPYDLVLME-GKMNYICTTGOMARRSYLGAVFNLTADHL 258
QY 289 SIOVSNPSILDPODATYFGAPKV 312
DB 259 YVNWSLSLVNFEEESTKFELYKL 282

RESULT 12
TNF6_MACMO STANDARD; PRT; 280 AA.

AC Q9MLG6; Q9BDM5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Macaca mulatta (Rhesus macaque);
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey); and
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
ap SEQUENCE FROM N.A.
IC SPECIES=M.mulatta; TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., Kling C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
FT Immunogenetics 53:315-328(2001).
RL [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RA Kiril Y., Inoue T., Yoshino K.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
modulates its effects (By similarity).
CC -1- SUBUNIT: Homotrimer (Potential).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
similarity).
CC -1- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; AF344856; AAK37539.1; -
EMBL; AB035138; BAA90294.1; -
EMBL; AB035139; BAA90295.1; -
EMBL; AB035140; BAA90296.1; -
HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 280
FT CHAIN 129 280
FT CHAIN 1 80
FT DOMAIN 81 101
FT TRANSMEM 81 101

FT FT DOMAIN 102 280 (POTENTIAL).
FT FT DOMAIN 4 69 EXTRACELLULAR (POTENTIAL).
FT FT DOMAIN 45 64 PRO-RICH.
FT SITE 128 129 POLY-PRO.
FT DISULFID 201 232 CLEAVAGE (BY SIMILARITY).
FT CARBOHYD 183 183 POTENTIAL.
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
Query Match 10.68; Score 178; DB 1; Length 280;
Best Local Similarity 22.08; Pred. No. 1.4e-07;
Matches 68; Conservative 44; Mismatches 105; Indels 92; Gaps 10;
QY 22 PGVPEGHLPAPAPAP--APPAAASRS-----MFLALGLGLGQWVCSI 65
DB 46 PPPPPPPPLPPPPSPPLPLPLPKKRNHSTGLCLVMEFVNLVALVGLGLG----- 99
QY 66 ALFLYFRACMDPNRISESTHCFYRLILRHENAGLQDSTLESDTLPSCRMRKQAFGA 125
DB 100 -MFQLFHLQ-----KELAELESTSQKHTA-----SS 125
QY 126 VQELQHLVIGVQRFSGAPAMEGSWLDVAQRCKPAQFAHLT--INAAIPSGSHKVTL 183
DB 126 LEKQIGHFSPPE-----KKQRVAHLTGKPNRSM----- 158
QY 184 SSWYHGRGWAKISNMTLSNGLRVNODGFYLYANICFRHETSGVPTDYQLQMVYVK 243
DB 159 LEWEDTYGLVLSGVYKKGGLVINETGLYFYKSVFQGQCTN-----LPLSHKVYM 212
QY 244 TSIRKPSHNLKGGSTKNSGSEFHYFYSINVGFFKLRAGEEISIQVSNPDLDPDQD 303
DB 213 RSKYPQDLVWME-GKMSYCTTGQWVAHSSYLGAVFNLTSDHLYVNVSELSLVNFES 271
QY 304 ANYFGAFKV 312
DB 272 QTFFGLYKL 280
RESULT 13
TNF6_CERTO STANDARD; PRT; 280 AA.
AC Q9BDN1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TNFSF6 OR FASL OR CD95L.
OS Cercocobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercocobus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
CC -1- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/Dcr3
modulates its effects (By similarity).
CC -1- SUBUNIT: Homotrimer (Probable).

CC CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).

CC CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC CC EMBL: AF344847; AAK37606.1; 280

DR HSP: P01375; 4TSV.

DR InterPro: IPR003636; TNF_abc.

DR MEDLINE: 21383618; PubMed-11491335;

DR Pfam: PF00229; TNF_1.

DR PRINTS: PR01234; TNCRSISFCT.

DR PRODOM: PD002012; TNF_abc; 1.

DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF_1; 1.

DR PROSITE: PS0049; TNF_2; 1.

DR Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM.

FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 6, SOLUBLE FORM (BY SIMILARITY).

FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 81 101 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 102 280 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 4 69 PRO-RICH.

FT DOMAIN 45 64 POLY-PRO.

FT SITE 128 129 CLEAVAGE (BY SIMILARITY).

FT DISULFID 201 232 POTENTIAL.

FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match 10.6%; Score 177; DB 1; Length 280;

Best Local Similarity 21.3%; Pred. No. 1.6e-07;

Matches 67; Conservative 43; Mismatches 107; Indels 98; Gaps 9;

QY 22 PGVPEGLHPAPAPAPAPAPAPASRM-----FLALLGLGLG 59

DB 40 PGORPPPPPPPPPPPPPPPPPPPPPLPLPLPLPKKRNHSTGCLLYMFFVVALVGLGLG 99

DB 60 QVVCSTALYLPRAQMDPNRIESTDTHCYRILRLHENAQLQDSTLESDTLPDSCRRMK 119

DB 100 -----MFQFLHQ-----KELAELESTSQKHTA----- 123

QY 120 QAFQAGVQELAHIVGPQFSCAPAMEGSWLDVAQGPPEAPPAHLT--INAAISPSG 177

DB 124 -----SLKQIGHPPPP-----KKEQKVAHLTGKPNRSMP-- 158

QY 178 SHKVTLSHYDRGWAKISNMTLSNKLKRVNDGFFLYANICFRHETSGSVPTDYQLQ 237

DB 159 -----LEWEDYIGVILLGVKKGLVINETGLYFVYSKYVFRQSCSTN-----LPL 206

QY 238 MYVVKTSIKIPSSNHLKGGSTKNWGNSEPHFYSINVGFFKLKRGAEISIQVNSPL 297

DB 207 SHKVTMRNSKYPQDLVME-GKMMSYCTTGQMAHSSYLGAVENTLTSTDLHYVNVSELS 265

QY 298 LPPQDQATYEGAFV 312.

DB 266 VNFESQTFGLYKL 280

RESULT 14

TNF5_MACMU

ID AC TNF5_MACMU STANDARD; PRT; 261 AA.

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-

DE L) (CD154 protein).

GN TNFSF5 OR CD40LG OR CD40L.

OS Macaca mulatta (Rhesus macaque), and

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopitheinae; Macaca.

OX NCBI_TaxID=9544, 9531;

RN [1]

RP SEQUENCE FROM N.A., AND M.MULATTA VARIANTS GLN-60; VAL-204; PRO-206 AND THR-215.

RC SPECIES-M.mulatta, and C.torquatus atys; TISSUE-Lymphocytes;

EX MEDLINE-21383618; PubMed-11491335;

RA Villinger F., Postik P., Wayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;

RT "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules.";

RL Immunogenetics 53:315-328(2001).

CC -1- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).

CC -1- SUBUNIT: Homotrimer (By similarity).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an extracellular soluble form (By similarity).

CC -1- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC EMBL: AF344859; AAK37541.1; --

DR EMBL: AF344841; AAK37600.1; --

DR HSP: P29965; ITALY.

DR InterPro: IPR003263; TNF_5.

DR InterPro: IPR003636; TNF_abc.

DR InterPro: IPR000478; TNF_family.

DR Pfam: PF00229; TNF; 1.

DR PRODOM: PD002012; TNF_abc; 1.

DR PRODOM: PD008600; TNF_5; 1.

DR SMART: SM00207; TNF; 1.

DR PROSITE: PS00251; TNF_1; 1.

DR PROSITE: PS0049; TNF_2; 1.

KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Polymorphism.

FT CHAIN 1 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, MEMBRANE FORM.

FT CHAIN 113 261 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY).

FT DOMAIN 1 22 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 23 43 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 44 261 EXTRACELLULAR (POTENTIAL).

FT SITE 112 113 CLEAVAGE (BY SIMILARITY).

FT DISULFID 178 218 POTENTIAL.

FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 60 60 H -> Q (IN M.MULATTA).

FT VARIANT 204 204 I -> V (IN M.MULATTA).

FT VARIANT 206 206 L -> P (IN M.MULATTA).

FT VARIANT 215 215 A -> T (IN M.MULATTA).

CC SEQUENCE 261 AA; 29366 MW; AA2E0F11C0F28ABB CRC64;

RESULT 15

1	ID	TNF6_HUMAN	STANDARD:	PRT;	281 AA.
2	AC	P48203; Q9BP29;			
3	DC	01-FEB-1996 (Rel. 33, Created)			
4	DT	01-FEB-1996 (Rel. 33, Last sequence update)			
5	DT	15-JUN-2002 (Rel. 41, Last annotation update)			
6	DE	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)			
7	DE	(Apoptosis antigen ligand) (APTL) (CD178 antigen).			
8	GN	TNFSF6 OR FASL OR APTL1.			
9	OS	Homo sapiens (Human).			
10	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
11	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
12	OX	NCBI_Taxid=9606;			
13		[1]			
14	SEQUENCE FROM N.A. (ISOFORM 1).				
15	MEDLINE=95105731; PubMed=7528780;				
16	RA	Allderson M.;			
17	RT	"Fas ligand mediates activation-induced cell death in human T			
18	RT	lymphocytes.";			
19	RL	J. Exp. Med. 181:71-77(1995).			
20	LN	[2]			
21	SEQUENCE FROM N.A. (ISOFORM 1).				
22	MEDLINE=95127560; PubMed=7826947;				
23	RA	Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;			
24	RT	"Human Fas ligand: gene structure, chromosomal location and species			
25	RT	specificity.";			
26	RL	Int. Immunol. 6:1567-1574(1994).			
27	LN	[3]			
28	SEQUENCE FROM N.A. (ISOFORM 1).				
29	RA	Schaezelin C.E., Poehlmann R., Philippssen P., Eibel H.;			
30	RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.			
31	LN	[4]			
32	SEQUENCE FROM N.A. (ISOFORM 1).				
33	MEDLINE=95071350; PubMed=7980502;				
34	RA	Mita E., Hayashi N., Iio S., Takehara T., Hijioaka T., Kasahara A.,			
35	RA	Fusamoto H., Kamada T.;			
36	RT	"Role of Fas ligand in apoptosis induced by hepatitis C virus			
37	RT	infection.";			
38	RL	Biochem. Biophys. Res. Commun. 204:468-474(1994).			
39	LN	[5]			
40	SEQUENCE FROM N.A. (ISOFORM 2).				
41	TISSUE=Leukocyte.				
42	RA	Zeytun A., Nagarkatti M., Nagarkatti P.S.;			
43	RT	"Isolation and characterization of a new naturally occurring variant of			
44	RT	human Fas ligand that is expressed only in membrane bound form.";			
45	RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.			
46	LN	[6]			

SEQUENCE FROM N.A.
Wilkinson J.;
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Blood;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 1-10 FROM N.A.
TISSUE=Blood;
Matsumura M.; Nakanishi Y., Ohba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
[9]
CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
PubMed-9228058;
Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
Tersklth A., Reitsch M.C., Tschopp J.;
"Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
J. Biol. Chem. 1272:18827-18833(1997).
[10]
PROCESSING.
PubMed-9427603;
Tanaka M., Itai T., Adachi M., Nagata S.;
"Downregulation of Fas ligand by shedding.";
Nat. Med. 4:31-36(1998).
-I- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
modulates its effects.
-I- SUBUNIT: HOMOPRIMER (PROBABLE).
-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
SURFACE.
-I- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2;
are produced by alternative splicing.
-I- PTM: N-glycosylated.
-I- PTM: The soluble form derives from the membrane form by
proteolytic processing.
-I- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS), also known as Canale-Smith
syndrome (CSS), a childhood syndrome involving hemolytic anemia
and thrombocytopenia with massive lymphadenopathy and
splenomegaly.
-I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-I- DATABASE: NAME=PROW; NOTE=PROW 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/3338769674.g.htm".

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or send an email to license@isb-sib.ch).

EMBL; X89102; CAA61474.1; --
EMBL; U08137; AAC50071.1; --
EMBL; U11821; AAC50124.1; --
EMBL; D38122; BAA07320.1; --
EMBL; AF288573; AAG60017.1; --
EMBL; Z36050; CAB09424.1; --
EMBL; BC017502; AAI17502.1; --
EMBL; AB013303; BAA32542.1; --
HSP; P01375; ITNE.
Genew; HGNC:11936; TNFSF6.
MIM; 134636; --
MIM; 601859; --
InterPro; IPR003636; TNF-abc.
InterPro; IPR000478; TNF family.

Search completed: April 16, 2003, 12:19:00
Job time : 10.5 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 16, 2003, 12:16:42 ; Search time 28 Seconds
(without alignments)
2325.389 Million cell updates/sec

Title: US-09-787-126-6

Perfect score: 1675

Sequence: 1 MRRASRDYGYKLSSEMGs.....LLPDDQATYFGAFKVDID 316

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	263.5	15.7	214	13 Q9DDZ5	Q9ddz5 brachydanio
2	217.5	13.0	287	13 Q90WT9	Q90wt9 gallus gall
3	149	8.9	234	6 Q9TTJ3	Q9ttj3 equus caball
4	142	8.5	232	4 Q9UIV3	Q9uiv3 homo sapien
5	133.5	8.0	215	11 Q99ND1	Q99nd1 tamiasciuru
6	133	7.9	157	4 Q43647	O43647 homo sapien
7	132	7.9	149	6 Q97543	Q97543 actus nancy
8	132	7.9	217	11 Q9ERG6	Q9erg6 peromyscus
9	131.5	7.9	156	11 Q91ZL4	Q91zl4 sigmodon hi
10	131	7.8	149	6 Q97538	Q97538 actus vocif
11	131	7.8	149	6 Q97T68	Q97t68 actus nigri
12	130	7.8	216	11 Q70332	Q70332 mesocricetu
13	127.5	7.6	217	6 Q9BEC5	Q9bec5 tenrec ecan
14	126.5	7.6	217	6 Q9BEG1	Q9beg1 bradypus tr
15	126.5	7.6	217	6 Q9BEG0	Q9beg0 cyclopes di
16	126	7.5	216	6 Q9BEC9	Q9bec9 ochotona pr

17	125.5	7.5	235	11 Q9J127	Q9j127 rattus norv
18	123.5	7.4	138	6 Q9TTG7	Q9ttg7 actus lemur
19	122.5	7.3	215	6 Q9BEE8	Q9bee8 erinaceus e
20	122.5	7.3	235	11 Q9J126	Q9j126 rattus norv
21	120.5	7.2	217	6 Q9BEP4	Q9bef4 cabassous u
22	118.5	7.1	216	6 Q9BEC4	Q9bec4 talpa europ
23	114.5	6.8	432	11 Q9ESV6	Q9esv6 rattus norv
24	103	6.1	3848	5 Q76737	Q76737 dictyosteli
25	102	6.1	169	11 Q9WV90	Q9wv90 marmota mon
26	101.5	6.1	246	13 Q9I976	Q9i976 oncorhynch
27	101.5	6.1	246	13 Q9I970	Q9i970 oncorhynch
28	101.5	6.1	962	16 Q8XX7	Q8xx7 ralstonia s
29	101	6.0	216	6 Q9BEE0	Q9bee0 macropus ru
30	100.5	6.0	551	6 Q8WP18	Q8wp18 macaca fasc
31	100.5	6.0	1014	6 Q8WP17	Q8wp17 macaca fasc
32	99.5	5.9	558	5 Q45692	Q45692 caenorhabdi
33	97	5.8	255	13 Q9DEP9	Q9dep9 oncorhynch
34	97	5.8	325	5 Q9V5G2	Q9v5g2 drosophila
35	96	5.8	408	16 Q98LN7	Q98ln7 rhizobium l
36	96	5.7	1485	13 Q91717	Q91717 xenopus lae
37	95	5.7	1012	4 Q9UER7	Q9uef7 homo sapien
38	94	5.6	891	1 Q93635	Q93635 thermococcu
39	93	5.6	93	6 Q9TTJ2	Q9ttj2 bos taurus
40	92.5	5.5	214	6 Q9BEE3	Q9bef3 didelphis m
41	92	5.5	294	2 Q53921	Q53921 synechococc
42	92	5.5	549	4 Q9Y4F0	Q9y4f0 homo sapien
43	92	5.5	785	5 Q9XUS7	Q9xus7 caenorhabdi
44	92	5.5	1012	4 Q9UEI9	Q9uei9 homo sapien
45	91	5.4	218	11 Q9DAT2	Q9dat2 mus musculu

ALIGNMENTS

RESULT 1

Q9DDZ5 PRELIMINARY; PRT; 214 AA.

AC Q9DDZ5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE TRAIL-like protein.
GN TNFSF10L.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_taxid=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Bobe J., Goetz F.W.;

RT "Molecular cloning and expression of a TNF receptor and two TNF

ligands in the fish ovary."

RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).

DR EMBL; AF250041; AAG47640.1;

DR HSSP; P50591; IDOG.

DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.

DR InterPro; IPR003636; TNF_abc.

DR Pfam; PF00229; TNF; 1.

DR ProDom; PD002012; TNF_abc; 1.

DR SMART; SM00207; TNF; 1.

DR PROSITE; PS00049; TNF_2; 1.

SQ SEQUENCE. 214 AA; 24093 MW; 98C002474FF691AA CRC64;

Query Match 15.7%; Score 263.5; DB 13; Length 214;

Best Local Similarity 31.5%; Pred. No. 3.3e-15;

Matches 69; Conservative 42; Mismatches 77; Indels 31; Gaps 6;

QY 117 RKQAFQAGVAVQKELQHVGPQRFSGAPAMNE-----GS--WLDVAGQGRKPEAQAHLTI 169

DB 2 KLAEGIKAYISKVTDISIISKQTLHAARTQTHSYNTGSKFNTVMQR-----PSAHLTL 55

QY 170 NAASIPS-----GSHKVTLSWYHGRWAKISNMTLSNGKLRVNDQFYFL 215
 DB 56 SSASNSRQSDMHQPOFDLHSCRPVHTWANKFGLHYNTLNGKLRVNDQFYFL 115
 QY 216 YANICFRHETSGVPTDYQLQMLVYV--KTSIKIPSSHNLMKGGSTKNWNSSEFHYFS 273
 DB 116 YSQVTFYRPSDSQSSVSHQVLCYKTKSYLNP1--QLLKGVTGTCWAPDAEVALHS 173
 QY 274 INVGGFKLRAGEEISIOVSNPLDPPDQATYFCAKV 312
 DB 174 VTQGLFLRAGDEVFVSSTPMYIGEDSSSYFCAFRL 212

RESULT 2
 Q90WT9 PRELIMINARY; PRT; 287 AA.
 ID Q90WT9
 AC Q90WT9;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 Gallus gallus (Chicken).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bridgman J.T., Johnson A.L.;
 RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen
 ovary."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY057941; AAL23702.1;
 DR InterPro: IPR003636; TNF_family.
 DR ProDom: IPR000478; TNF_abc.
 DR Pfam: PF00229; TNF; 1.
 DR ProDom: PD02012; TNF_abc; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32092 MW; DB06ELC95087B108 CRC64;

Query Match 13.0%; Score 217.5; DB 13; Length 287;
 Best Local Similarity 26.7%; Pred. No. 5.4e-11;
 Matches 66; Conservative 51; Mismatches 103; Indels 27; Gaps 8;

QY 81 SEDSTHCFYRILRLHNLNAGLDSTLESDTLFDCRRMKQAFQAGVQKELHIVGPQFES 140
 DB 51 SSELRCILQINQOEGNLEE--LISN---QSCILKANTIKAYVATVTENVISRSYVN 104
 QY 141 GAPAMEGSWLDVAQ---RGKPEAQPFALHTI---NAASIPSG-----SHKVTLSW 186
 DB 105 EA---QKSYFNISEGVATYTLGRPSAHLFRPQNPADGSSRRFGLNLSQSRHAITRW 160
 QY 187 YHGRWAKISNMTLSNGKLRVNDQFYFLYANICFRHETSGVPTDYQLQMLVYV-VKTS 245
 DB 161 EDSTHSHLONITRDGLRLVNDQFYFLYANICFRHETSGVPTDYQLQMLVYV-VKTS 220
 QY 246 IKIPSSHNLMKGGSTKNWNSSEFHYFSINVGKPKLAGEISIOVSNPLDPPDQAT 305
 DB 221 YSQPL--LLKGVTGTCWAPDAEYGLHALYOGGLFELKAGDELFSVSSLAIDYSDAAS 278
 QY 306 YFGAFKV 312
 DB 279 YFGAFRL 285

RESULT 3
 Q9TTJ3 PRELIMINARY; PRT; 234 AA.
 ID Q9TTJ3
 AC Q9TTJ3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor-alpha.

GN TNFA.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=THOROUGHRED; TISSUE=ARTERIAL ENDOTHELIUM;
 RA Ishida N., Sato F., Hasegawa T.;
 RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB035735; BAA88349.1;
 DR HSSP: P01375; 188M.
 DR InterPro: IPR003636; TNF_abc.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR PRINTS: PR01234; TNECROSISFCT.
 DR ProDom: PD02012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 DR PROSITE: PS0049; TNF_2; 1.
 SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

Query Match 8.9%; Score 149; DB 6; Length 234;
 Best Local Similarity 24.18; Pred. No. 4.1e-05;
 Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

QY 133 IVGPQFSGAPAMEGSWLDVAQKQ-----PEAQPFALHTINAASIPSGSHKVTLSWY 187
 DB 55 VIGPQREQLPNAQF-SINPLAQLTSSRTSPDFVAHVAN-----PQAEGL---QWL 106
 QY 188 HDRGWAKISN-MTSLNGKLRVNDQFYFLYANICFRHETSGVPTDYQLQMLVYVVKTSI 246
 DB 107 SGRANALLANGVKLTDLNQLVPLDGLYLYSOVLEK---GQCPCSTHVLTHITISRLAV 162
 QY 247 KIPSSHNLMKG-----GSTKNWNSSEFHYFSINVGKPKLAGEISIOVSN 294
 DB 163 SYPSKVNLLSAIKSLANTESPQAEAKPW-----YEPIYLGGVQLEKGDLSABINQ 215
 QY 295 PSLLD-PPDQATYFG 308
 DB 216 PNYLDFAESGGVYFG 230

RESULT 4
 Q9UIV3 PRELIMINARY; PRT; 232 AA.
 ID Q9UIV3
 AC Q9UIV3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Tumor necrosis factor.
 GN TNF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93272029; PubMed=8499947;
 RA Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot V.,
 RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
 RT "Dense Alu clustering and a potential new member of the NFkappaB
 family within a 90 kilobase HLA class III segment."
 RL Nat. Genet. 3:137-145(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96215741; PubMed=8629302;
 RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
 RA Wallace A.F., Russell M.E.;
 RT "Allograft inflammatory factor-1. A cytokine-responsive macrophage
 molecule expressed in transplanted human hearts."
 RL Transplantation 61:1387-1392(1996).


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097543
ID AC 097543 PRELIMINARY; PRT; 149 AA.
DT 01-MAY-1999 (TEmBLrel. 10, Created)
DT 01-MAY-1999 (TEmBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TEmBLrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotidae; Aotus.
OC NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Scheverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.
RT "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species."
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014513; AAD01539.1; -
DR HSP; P01375; tsv.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF.1; 1.
DR PROSITE; PS50049; TNF.2; 1.
FT NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16466 MW; 3C2A6140778EFABA CRC64;

Query Match 7.9%; Score 132; DB 6; Length 149;
Best Local Similarity 24.4%; Pred. No. 0.00068;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps

QY 159 PEAPPFAPHLRNAASIPSGSHKVTLSWSHRCWAKISN-MTLSNGLRVNODGFYLYA 217
Db 1 PSDEPVAHVAVN-----PQAGQL---QWLNRANALLANGVELRDQLVVPSEGLYLI 53
QY 218 NICFRHETSGSVPTDYQL-----MVYVVK-----TSIKIPSHNLMKGSITKNWSG 265
Db 54 QVLFPK-----GQGFSTHVLTHITRIASVSYQTKVLLSAIKSPQCRTEPGAERKPW-- 197
QY 266 NSEFHYSINVGFFKLRAAGEEISIOVNSPFLSD-PDQDATVFG 308
Db 108 -----YEPYILGVVQLERGLRSLAENRPDYLDFAESQGVFG 146

RESULT 8
Q9ERG6 PRELIMINARY; PRT; 217 AA.
ID AC Q9ERG6 PRELIMINARY; PRT; 217 AA.
DT 01-MAR-2001 (TEmBLrel. 16, Created)
DT 01-MAR-2001 (TEmBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TEmBLrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OC NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
necrosis factor genes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; AAG30264.1; -
DR HSP; P66804; TNF.
DR InterPro: IPR003636; TNF_abc.
DR InterPro: IPR000478; TNF_family.

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DR Pfam: PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match
Best Local Similarity 7.9%; Score 132; DB 11; Length 217;
Matches 46; Conservative 31; Mismatches 68; Indels 44; Gaps 8;

QY 133 IVGQRFSGAP-----AMEGSWLDVAGRGKPEAQPFAHLTINAASIPSGSHKVTLS-184
DB 47 VIGQREEFPPNLPITGSAQTLTLRSSQSSD-KPVAHVAN-----HQVDEQL 97

185 SMYHDSRGWAKISN-WTSLNGKLRVNDGFFYLYVANTICFRHETSGSVPTDYQLAVYVVK 243
DB 98 EWLSSRRANALLANGMDLKNOLVIPADGLYLVYSQVLFKGGGCSNVY-----LLRHTVS 151

QY 244 -----TSIKIPSSHNLKMGSTKWSGSEHFEYINVGPFKLAGEEISI 290
DB 152 RFVSYEDKVNLSAISKPCPKETPEGSELKPW-----YEPIYLGGVFQLEKGRDLSA 204

QY 291 QVSNPSLLD 299
DB 205 EVNLPKYLVD 213

RESULT 9
QY1ZL4 PRELIMINARY; PRT; 156 AA.
ID Q91ZL4
AC Q91ZL4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Sigmomon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmomoninae;
OC Sigmomon.
OX NCBI_TaxID=42415;
RN [1]
RP SEQUENCE FROM N.A.
AL Blanco J.C., Pieteva L.M., Prince G.A.;
AL "Sigmomon hispidus cytokines, chemokines and interferons.";
AL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421388; AAL1818.1;
DR InterPro; IPR003636; TNF; 1.
DR InterPro; IPR000478; TNF; 1.
DR Pfam; PF00229; TNF; 1.
DR PRODOM; PD002012; TNF; 1.
DR PROSITE; PS00251; TNF_1; UNKNOWN_1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 156 AA; 17303 MW; DC565F3BC3C82684 CRC64;

Query Match
Best Local Similarity 7.9%; Score 131.5; DB 11; Length 156;
Matches 39; Conservative 27; Mismatches 61; Indels 35; Gaps 6;

QY 162 OPAHLTINAASIPSGSHKVTLSWYHDSRGWAKISN-WTSLNGKLRVNDGFFYLYANIC 220
DB 11 KPVAHVYVNAQAEQ-----LEWLSQRANALLANGMDLKNOLVIPADGLYLVYSQVL 63

QY 221 FRHETSGSVPTDYQLAVYVVK-----TSIKIPSSHNLKMGSTKWSGNS 267
DB 64 FK-----GLGRSCNELLTHVTSRIAVSYEDKVNLSAISKPCPKETPQGAELKPW----- 113

QY 268 EFHETSGSVPTDYQLAVYVVK-----TSIKIPSSHNLKMGSTKWSGNS 267
DB 64 FK-----GLGRSCNELLTHVTSRIAVSYEDKVNLSAISKPCPKETPQGAELKPW----- 113

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Db 114 ----YEPIYLGGVFQLEKGRDLSAENVNPKYLDPAESGQVYFG 152

RESULT 10
QY7538 PRELIMINARY; PRT; 149 AA.
ID Q97538
AC Q97538;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
AL Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
AL "Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.";
AL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014508; AAD01534.1;
DR HSSP; P01375; 4TSV.
DR InterPro; IPR003636; TNF; 1.
DR InterPro; IPR000478; TNF; 1.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODOM; PD002012; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match
Best Local Similarity 7.8%; Score 131; DB 6; Length 149;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAPPAHLTINAASIPSGSHKVTLSWYHDSRGWAKISN-WTSLNGKLRVNDGFFYLYA 217
DB 1 PSDKPAHVYVNAQAEQ-----PQAGQL-----OWLNRANALLANGVELNDQVLPSEGLYLVIS 53

QY 218 NICFRHETSGSVPTDYQLAVYVVK-----TSIKIPSSHNLKMGSTKWSGNS 265
DB 54 QVLFK-----GQCGPSTFMTLTHSIRIAVSQAKVNLSAISKPCQRETTPRGAKTNPW-- 107

QY 266 NSRFHETSGSVPTDYQLAVYVVK-----TSIKIPSSHNLKMGSTKWSGNS 265
DB 108 -----YEPIYLGGVFQLEKGRDLSAENVNPKYLDPAESGQVYFG 146

RESULT 11
QY7TGS PRELIMINARY; PRT; 149 AA.
ID Q97TGS
AC Q97TGS;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
GN TNF-ALPHA.
OS Aotus nigricaps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
AL Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
AL Patarroyo M.E.;
AL "Aotus nigricaps gene for TNF alpha.";
AL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF097328; AAF21303.1;
DR
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DR HSP: P01375; 4TSV
DR InterPro: IPR003636; TNE_abc.
DR InterPro: IPR000478; TNE_family.
DR Pfam: PF00229; TNE; 1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNE_abc; 1.
DR SMART: SM00207; TNE; 1.
DR PROSITE: PS00251; TNE_1; 1.
DR PROSITE: PS00049; TNE_2; 1.
DR NON_TER 1
FT NON_TER 149
SQ SEQUENCE 149 AA; 16415 MW; 86F1B9BCED16E689 CRC64;

Query Match 7.8%; Score 131; DB 6; Length 149;
Best Local Similarity 24.4%; Pred. No. 0.00084;
Matches 40; Conservative 31; Mismatches 61; Indels 32; Gaps 8;

QY 159 PEAOFPFAHITINAAISPGSGSHKVTLSWYHGRGAKISN-WTLSNGKLRVNDGFFYLVA 217
Db 1 PSDKPAHVAVN---PQEGQL---QWLNRRNALLANGVELRDNLVVPSEGLYLVIS 53
218 NICFRHETSGVPTDYLQ-----MVYVVK-----TSIKIPSSHNLKMGSGTKNWSG 265
54 QVLEK-----GQCPSTFMLTHSIRIAVSQAQVNLISAIRKPCQRETGRGAKTNPW-- 107
266 NSEFHYISNVGFFKLRAGEISIQVSNPSLLD-PQDQATVFG 308
108 -----YEPIYLGVOLEKGRLSAEINLPDYLDAESGVYTFG 146

RESULT 12
O70332 PRELIMINARY: PRT: 216 AA.
AC O70332;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tyron V.V., Chandrasekar B., Freeman G.L.;
RT Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis. Infect. Immun. 66:2135-2142(1998).
DR EMBL: AF046215; AAC40100.1; -.
DR HSP: P06804; 2TNE.
DR InterPro: IPR003636; TNE_abc.
DR InterPro: IPR000478; TNE_family.
DR Pfam: PF00229; TNE; 1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNE_abc; 1.
DR SMART: SM00207; TNE; 1.
DR PROSITE: PS00251; TNE_1; 1.
DR PROSITE: PS00049; TNE_2; 1.
DR NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;

Query Match 7.8%; Score 130; DB 11; Length 216;
Best Local Similarity 24.7%; Pred. No. 0.0017;
Matches 46; Conservative 29; Mismatches 71; Indels 40; Gaps 8;

QY 133 IVGPQRFSGAPAMMEGSLDVA---AQRKPEAQPFALHTINAASIPSGSHKVTLS-SWY 187
Db 47 VIGPQREKFPPIIGSMQTLTRSSQNSNDKPGHVAVN-----HQVEGLEWL 98

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QY 188 HDGRGAKISN-WTLSNGKLRVNDGFFYLIAICFRHETSGVPTDYLQLVYVVK--- 243
Db 99 SHRNALLANGSLKDNQIVPADGLYLVISQVLF-----GQCPSTYV-LTHVTVSRIA 152
QY 244 -----TSIKIPSSHNLKMGSGTKNWSGSEFHFYSINVGGFFKLRAGEEISIQVS 293
Db 153 VSYEDNVNLLSAIKSPCKETPEGEELKPW-----YEPIYLGVOLEKGRLSAEIN 205
QY 294 NPSLLD 299
Db 206 LPKYLID 211

RESULT 13
Q9BEC5 PRELIMINARY: PRT: 217 AA.
AC Q9BEC5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Tenrec ecaudatus (tailless tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Tenrec.
OX NCBI_TaxID=94439;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
their sister group.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ286826; CAC28538.1; -.
DR HSP: P01375; 4TSV.
DR InterPro: IPR003636; TNE_abc.
DR InterPro: IPR000478; TNE_family.
DR Pfam: PF00229; TNE; 1.
DR PRINTS: PRO1234; TNECROSISFCT.
DR ProDom: PD002012; TNE_abc; 1.
DR SMART: SM00207; TNE; 1.
DR PROSITE: PS00251; TNE_1; 1.
DR PROSITE: PS00049; TNE_2; 1.
DR NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 23845 MW; 1C5013E9B77B54A CRC64;

Query Match 7.6%; Score 127.5; DB 6; Length 217;
Best Local Similarity 24.0%; Pred. No. 0.0028;
Matches 49; Conservative 29; Mismatches 51; Indels 75; Gaps 10;

QY 133 IVGPQRFSGAPAMMEGSLDVAQRKPEAQ-----PFAHLTINAASIPSGSHK 180
Db 46 VIGPQREKFP-----GSPHLI-----KPLTQTLRSSRTSLDKPAHVAVV--ASTQDSGLK 95
QY 181 VTLSWYHGRG-AKISNWTLSN-----GKLRVNDGFFYLIAICFRHETSGSVPTD 233
Db 96 -----WVKYANALLDNVQLIDNLPDGLYLVISQVLFKPGCHGT----- 140
QY 234 YLQLVYVVKT-----SIKIPSSHNLKMGSGTKNWSGSEFHFYSIN 275
Db 141 -----YVILTHVTSRIASVQAQVNLISAIRKPCRETPESETKPV-----YEPIY 187
QY 276 VGGFFKLRAGEEISIQVSNPSLLD 299
Db 188 LGGVFOLQKGRLSAEINLPNYLD 211

RESULT 14
Q9BEG1 PRELIMINARY: PRT: 217 AA.
AC Q9BEG1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)

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RESULT 15
Q9BEGO
ID Q9BEGO PRELIMINARY; PRT; 217 AA.
AC Q9BEGO;
DT 01-JUN-2001 (T=EMBLrel. 17, Created)
DT 01-JUN-2001 (T=EMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (T=EMBLrel. 19, Last annotation update)
DE Tumor necrosis factor (Fragment).
GN TNFA.
OS Cyclopes didactylus (silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Edentata; Myrmecophagidae; Cyclopes.
OX NCBI_TaxId=84074;

[1]
RN SEQUENCE FROM N.A.
RP van Dijk M.A.M., de Jong W.W.;
RT *ndels indicate that rodents are monophyletic and lagomorphs are
RL their sister group.*;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286828; CAC28514.1; -.
DR HESP; F01375; IABM.
DR DR InterPro; IPR003636; TNF_abc.
DR DR InterPro; IPR000478; TNF_family.
DR DR Pfam; PF00229; TNF. 1.

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Search completed: April 16, 2003, 12:20:04
Job time : 29 secs

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 12:17:27 ; Search time 13.5 Seconds
(without alignments)
688.714 Million cell updates/sec

Title: US-09-787-126-6
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSSEMGSGPVHGPPLHPPAPSAFAPPPAASRSMFLALGLIGLQ 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	2	US-08-842-842-7
2	1675	100.0	316	4	US-08-989-362-2
3	1675	100.0	316	4	US-09-052-521C-2
4	1554	92.8	294	3	US-08-996-139-11
5	1554	92.8	294	4	US-08-995-659-11
6	1554	92.8	294	4	US-09-215-649A-11
7	1554	92.8	294	4	US-09-577-780-11
8	1417.5	84.6	317	3	US-08-996-139-13
9	1417.5	84.6	317	4	US-08-995-659-13
10	1417.5	84.6	317	4	US-09-215-649A-13
11	1417.5	84.6	317	4	US-09-052-521C-4
12	1417.5	84.6	317	4	US-09-577-780-13
13	258.5	15.4	279	4	US-09-072-993C-3
14	258.5	15.4	281	1	US-08-670-354-2
15	258.5	15.4	281	3	US-08-584-031-1
16	258.5	15.4	281	3	US-08-780-496-1
17	258.5	15.4	281	4	US-08-883-086-10
18	258.5	15.4	281	4	US-09-320-424-2
19	258.5	15.4	281	4	US-09-333-593A-6
20	258.5	15.4	281	4	US-09-157-864-11
21	258.5	15.4	281	5	PCR-US96-10895-2
22	244	14.6	291	1	US-08-670-354-6
23	244	14.6	291	4	US-09-320-424-6
24	244	14.6	291	5	PCR-US96-10895-6
25	240	14.3	256	4	US-09-320-424-13
26	236	14.1	253	4	US-09-320-424-11
27	229.5	13.7	177	4	US-09-105-343A-7

28 224 13.4 183 4 US-09-105-343A-8
29 183 10.9 278 4 US-08-339-214-16
30 183 10.9 278 4 US-08-339-214-26
31 182 10.9 279 4 US-08-339-214-24
32 182 10.9 279 4 US-08-339-214-32
33 173.5 10.4 281 2 US-08-810-453-2
34 173.5 10.4 281 3 US-08-815-190A-2
35 173.5 10.4 281 4 US-09-290-640-25
36 173.5 10.4 281 4 US-09-479-524-3
37 173.5 10.4 281 4 US-08-339-214-8
38 173.5 10.4 281 4 US-08-339-214-30
39 173.5 10.4 281 4 US-09-589-287B-6
40 173.5 10.4 281 4 US-09-157-864-10
41 173.5 10.4 281 4 US-09-006-755B-1
42 173.5 10.4 281 5 PCT-US95-00362-2
43 171.5 10.2 261 1 US-07-940-605A-2
44 171.5 10.2 261 1 US-08-184-423-8
45 171.5 10.2 261 1 US-08-360-923A-2

ALIGNMENTS.

RESULT 1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-842-7

Query Match 100.0%; Score 1675; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157; Indels 0; Gaps 0;
Matches 316; Conservative 0; Mismatches 0;

QY 1 MRRASRDYGYLRSSEMGSGPVHGPPLHPPAPSAFAPPPAASRSMFLALGLIGLQ 60
Db 1 MRRASRDYGYLRSSEMGSGPVHGPPLHPPAPSAFAPPPAASRSMFLALGLIGLQ 60
QY 61 VVCSIALFLYFRAQMDPNRISEDTCHFCYRILRLHFNAGLDQSTLESDTLPDSCRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDTCHFCYRILRLHFNAGLDQSTLESDTLPDSCRMKQ 120
QY 121 AFOGAVQKQLQHVGPORFSGAPAMMGSLDVAQRKPEAQPPAHLTINAASTPSGSHK 180
Db 121 AFOGAVQKQLQHVGPORFSGAPAMMGSLDVAQRKPEAQPPAHLTINAASTPSGSHK 180

QY 181 VTLSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQWY 240
DB 181 VTLSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQWY 240
QY 241 VVTSIKIPSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYGAFAKVQDID 316
DB 301 DQDATYGAFAKVQDID 316

RESULT 2

US-08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Mattson, Jeanine D.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; TITLE OF INVENTION: Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-989-362-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYGYLRSSEMGSGVPHGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
DB 1 MRRASRDYGYLRSSEMGSGVPHGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
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DB 61 VVCSIALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
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DB 121 AFOGAVOKELQHIYGVQPFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180

QY 181 VTLSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQWY 240
DB 181 VTLSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQWY 240
QY 241 VVTSIKIPSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYGAFAKVQDID 316
DB 301 DQDATYGAFAKVQDID 316

RESULT 3

US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451BIV
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIORITY APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mouse
; US-09-052-521C-2

Query Match 100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYGYLRSSEMGSGVPHGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
DB 1 MRRASRDYGYLRSSEMGSGVPHGPHLPAPSAPAPPPAASRSMFLALLGLGLGQ 60
QY 61 VVCSIALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
DB 61 VVCSIALFLYFRAQMDPNRIESTDTHCFYRILRLHENAGLQDSTLESDTLPDSCRRMKQ 120
QY 121 AFOGAVOKELQHIYGVQPFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180
DB 121 AFOGAVOKELQHIYGVQPFSCAPAMMGSLDVAORGKPEAQPPFAHLTINAASIPSGSHK 180
QY 181 VTLSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQWY 240
DB 181 VTLSWYHGRGAKISNNTLSNGKLRVNDGFFYYLIYANICFRHHETSGSVPTDYQLQWY 240
QY 241 VVTSIKIPSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPSLLDP 300
DB 241 VVTSIKIPSHNLKMGSTKNSGSEFFHYISINVGFFKLRAGEEISIQVSNPSLLDP 300
QY 301 DQDATYGAFAKVQDID 316
DB 301 DQDATYGAFAKVQDID 316

RESULT 4

US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene

US-09-215-649A-11
: Sequence 11, Application US/09215649A
: Patent No. 6271349
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: Galibert, Laurent
: Maraskovsky, Eugene
: TITLE OF INVENTION: Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/215,649A
: FILING DATE: 17-Dec-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/996,139
: FILING DATE: <Unknown>
: APPLICATION NUMBER: USN 08/813,509
: FILING DATE: 07 MARCH 1997
: APPLICATION NUMBER: USN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2851-A
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-215-649A-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQAVQKELQHVGPQFSGA 142
DB 61 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQAVQKELQHVGPQFSGA 120
QY 143 PAMMEGSLDVAORGPKEAPPAHLTINAASIPSGSHKVTLSWYHHRGWAKISNMTLSN 202
DB 121 PAMMEGSLDVAORGPKEAPPAHLTINAASIPSGSHKVTLSWYHHRGWAKISNMTLSN 180
QY 203 GKLVRNODGYIYLANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 262
DB 181 GKLVRNODGYIYLANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 240
QY 263 WSGNSEFHFTYSINVGFFFKLRAGEEISIQVSNPDLDPQDQDATYFFGAFKQVQDID 316
DB 241 WSGNSEFHFTYSINVGFFFKLRAGEEISIQVSNPDLDPQDQDATYFFGAFKQVQDID 294

RESULT 7
US-09-577-780-11
: Sequence 11, Application US/09577780
: Patent No. 6419929
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: Galibert, Laurent
: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/577,780
: FILING DATE: 24-May-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/995,659
: FILING DATE: <Unknown>
: APPLICATION NUMBER: USN 08/813,509
: FILING DATE: 07 MARCH 1997
: APPLICATION NUMBER: USN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELEPHONE: (206)587-0430
: TELEFAX: (206)233-0644
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 294 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-577-780-11

Query Match 92.8%; Score 1554; DB 4; Length 294;
Best Local Similarity 99.7%; Pred. No. 3.5e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 23 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE 82
DB 1 GVPHEGLHPAPAPAPPPAASRSMFLALLGLGQVVCSTALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQAVQKELQHVGPQFSGA 142
DB 61 DSTHCFYRILRLHENADLQDSTLESDTLPSDCRRMKQAFQAVQKELQHVGPQFSGA 120
QY 143 PAMMEGSLDVAORGPKEAPPAHLTINAASIPSGSHKVTLSWYHHRGWAKISNMTLSN 202
DB 121 PAMMEGSLDVAORGPKEAPPAHLTINAASIPSGSHKVTLSWYHHRGWAKISNMTLSN 180
QY 203 GKLVRNODGYIYLANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 262
DB 181 GKLVRNODGYIYLANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSNLMKGGSTKN 240
QY 263 WSGNSEFHFTYSINVGFFFKLRAGEEISIQVSNPDLDPQDQDATYFFGAFKQVQDID 316
DB 241 WSGNSEFHFTYSINVGFFFKLRAGEEISIQVSNPDLDPQDQDATYFFGAFKQVQDID 294

RESULT 8
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-996-139-13

Query Match 84.6%; Score 1417.5; DB 3; Length 317;
Best Local Similarity 84.3%; Pred. No. 1.1e-131;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLSSEEMSGPGVPHEGPHAPAPAPPPAASRSMFALLGLGLGQ 60
|||||
DB 1 MRRASRDYTKYLGSEEMGGPGAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 59
|||||

QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRLRLHENAGLDSTLESED-TPDSCRRM 118
|||||
DB 60 VVCSVALFFYFRAQMDPNRISEDTGTHCYRLRLHENADFDQTTLESQDTKLIPDSCRR 119
|||||

QY 119 KQAFQAVQKELQHIYGVQRFSGAPAMEGSWLDVAQRGKPEAQPFALHINAASIPSGS 178
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DB 120 KQAFQAVQKELQHIYGVQSHIRAKAVDGSWLDLAKRSKLEAQPFALHINATDIPSGS 179
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QY 179 HKVTLSSWYHRCWAKISNNTLSNGKLRVNDGFFYLYANICFRHHETSGVPTDYQLQM 238
|||||
DB 180 HKVTLSSWYHRCWAKISNNTFSGKLVNQDGFYLYANICFRHHETSGDLATEYLQLM 239
|||||

QY 239 VYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYTSINVGFFKLRSGEEISIEVSNPSLL 299
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Db 240 VYVTKTSIKIPSSHTLMKGGSTKYNWGNSEFHYTSINVGFFKLRSGEEISIEVSNPSLL 299

QY 299 DPQDATYFGAFKVDID 316
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Db 300 DPQDATYFGAFKVDID 317

RESULT 9
US-08-995-659-13
; Sequence 13, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,659
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-13

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
Best Local Similarity 84.3%; Pred. No. 1.1e-131;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLSSEEMSGPGVPHEGPHAPAPAPPPAASRSMFALLGLGLGQ 60
|||||

Db 1 MRRASRDYTKYLGSEEMGGPGAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 59
|||||

QY 61 VVCSIALFLYFRAQMDPNRISESTHCFYRLRLHENAGLDSTLESED-TPDSCRRM 118
|||||

Db 60 VVCSVALFFYFRAQMDPNRISEDTGTHCYRLRLHENADFDQTTLESQDTKLIPDSCRR 119
|||||

QY 119 KQAFQAVQKELQHIYGVQRFSGAPAMEGSWLDVAQRGKPEAQPFALHINAASIPSGS 178
|||||

119 HVKLTSSWYHDKGAKISNMNLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 120 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKRSKLEQAOPFAHLTINATDIPSGS 179
 179 HVKLTSSWYHDKGAKISNMNLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 180 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKRSKLEQAOPFAHLTINATDIPSGS 179
 239 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 298
 240 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 299
 299 DPQDATYGAFAKVDID 316
 300 DPQDATYGAFAKVRDID 317

RESULT 10

US-09-215-649A-13
 ; Sequence 13, Application US/09215649A
 ; Patent No. 6271349

GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.
 Galibert, Laurent
 Maraskovsky, Eugene
 TITLE OF INVENTION: Receptor Activator of NF-kappaB
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESS: Immunex Corporation, Law Department
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/215,649A
 FILING DATE: 17-Dec-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/813,509
 FILING DATE: 07 MARCH 1997
 APPLICATION NUMBER: USSN 08/772,330
 FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,693
 REFERENCE/DOCKET NUMBER: 2851-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206)587-0430
 TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
 LENGTH: 317 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-215-649A-13

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSGEEMSGGPGVHEGPHLPAPAPAPPPAAASRMFLALLGLGQ 60
 DB 1 MRRASRDYTKYLRSGEEMSGGPGVHEGPHLPAPAPAPPPAAASRMFLALLGLGQ 59

QY 61 VVCSIALFLYFRAQMDPNRISEDTHCFYRILRLHENAGLDSTLSEDT--LPDSCRM 118
 DB 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADQDTTLESQDTKLIPDSCRRI 119
 QY 119 KQAFQAVOKELQHIYVGPORFSGAPAMGSLDVAORGPEAPQFAHLTINAAISIPSGS 178
 DB 120 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKRSKLEQAOPFAHLTINATDIPSGS 179
 QY 179 HKVTLSSWYHDKGAKISNMNLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 DB 180 HKVTLSSWYHDKGAKISNMNLSNGKLRVNDGFFYLYANICFRHHETSGDLATEYLQLM 239
 QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 298
 DB 240 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYGAFAKVDID 316
 DB 300 DPQDATYGAFAKVRDID 317

RESULT 11

US-09-052-521C-4
 ; Sequence 4, Application US/09052521C
 ; Patent No. 6316408

GENERAL INFORMATION:

APPLICANT: Boyle, William J.
 TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
 FILE REFERENCE: A-4518rv
 CURRENT APPLICATION NUMBER: US/09/052,521C
 CURRENT FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 08/880,855
 PRIOR FILING DATE: 1997-06-23
 PRIOR APPLICATION NUMBER: 08/842,842
 PRIOR FILING DATE: 1997-04-16
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 4
 LENGTH: 317
 TYPE: PRT
 ORGANISM: Human
 US-09-052-521C-4

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
 Best Local Similarity 84.3%; Pred. No. 1.1e-131;
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSGEEMSGGPGVHEGPHLPAPAPAPPPAAASRMFLALLGLGQ 60
 DB 1 MRRASRDYTKYLRSGEEMSGGPGVHEGPHLPAPAPAPPPAAASRMFLALLGLGQ 59

QY 61 VVCSIALFLYFRAQMDPNRISEDTHCFYRILRLHENAGLDSTLSEDT--LPDSCRM 118
 DB 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADQDTTLESQDTKLIPDSCRRI 119
 QY 119 KQAFQAVOKELQHIYVGPORFSGAPAMGSLDVAORGPEAPQFAHLTINAAISIPSGS 178
 DB 120 KQAFQAVOKELQHIYVGSQHIRAEKAMVDGSLDLAKRSKLEQAOPFAHLTINATDIPSGS 179
 QY 179 HKVTLSSWYHDKGAKISNMNLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLM 238
 DB 180 HKVTLSSWYHDKGAKISNMNLSNGKLRVNDGFFYLYANICFRHHETSGDLATEYLQLM 239
 QY 239 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIOVSNPSLL 298
 DB 240 VYVTKTSIKIPSSHNLMKGGSTKNWGNSEFFHYFYSINVGFFKLRAGEEISIEVSNPSLL 299
 QY 299 DPQDATYGAFAKVDID 316
 DB 300 DPQDATYGAFAKVRDID 317

RESULT 12

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-2

Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.6e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
QY 43 PAASRSMFLALGLGIGVGVCSIALFLYFRAQMD--PNRISESTHCFYRLRLHENAGL 100
DB 10 PSIGQTCVLIVITVLLQSLCVAVTYVFTNELKQMDKYSGGIACF-----LKEDDSY 64
QY 101 QDSTLESEDTLPDCSRMRKQAFQGVOK-----ELQHVGPQFSGAPAMM 146
DB 65 WDP--NDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPL----- 113
QY 147 EGSWLDVAORGRPEAOPFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 114 -----VRENGPQVRA--AHITGRGRSNTLSPNKNKALGRKINSWESSRSGHFLS 165
QY 197 NMTLSNGKLVRNODGFYIYANICFRHHTSGSVPTDYQLQMWVYVVKTSIKIPSSHNLAK 256
DB 166 NLHLRNGELVIHEKGFYIYSQYFFRQOEIKENTNDQWQYIYKYT-SYDPDILLMK 224
QY 257 GGSTKNWGNSEPHFYISINVGGFFKLRAEIEISIQVSNPSSLDPDQDQATYFGAFV 312
DB 225 SARNSCWKDAEYGLYSIYGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFLV 280

RESULT 15
US-08-584-031-1
Sequence 1, Application US/08584031A
Patent No. 6030945
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred. No. 1.6e-17;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
QY 43 PAASRSMFLALGLGIGVGVCSIALFLYFRAQMD--PNRISESTHCFYRLRLHENAGL 100
DB 10 PSIGQTCVLIVITVLLQSLCVAVTYVFTNELKQMDKYSGGIACF-----LKEDDSY 64
QY 101 QDSTLESEDTLPDCSRMRKQAFQGVOK-----ELQHVGPQFSGAPAMM 146
DB 65 WDP--NDEESMNSPCQVQWQLRQLVRKMLRTSEETISTVQEKQONISPL----- 113
QY 147 EGSWLDVAORGRPEAOPFAHLT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS 196
DB 114 -----VRENGPQVRA--AHITGRGRSNTLSPNKNKALGRKINSWESSRSGHFLS 165
QY 197 NMTLSNGKLVRNODGFYIYANICFRHHTSGSVPTDYQLQMWVYVVKTSIKIPSSHNLAK 256
DB 166 NLHLRNGELVIHEKGFYIYSQYFFRQOEIKENTNDQWQYIYKYT-SYDPDILLMK 224
QY 257 GGSTKNWGNSEPHFYISINVGGFFKLRAEIEISIQVSNPSSLDPDQDQATYFGAFV 312
DB 225 SARNSCWKDAEYGLYSIYGGIFELKENDRIEIVSVTNEHLIDMDHEASFFGAFLV 280

Search completed: April 16, 2003, 12:21:16
Job time : 14.5 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 12:18:42 ; Search time 14.5 Seconds
(without alignments)
1647.861 Million cell updates/sec

Title: US-09-787-126-6
Perfect score: 1675
Sequence: 1 MRRASDYGYKLRSEMG.....LLDPQDQATYFGAKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 288829 seqs, 7561385 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	9 US-10-017-910-4	Sequence 4, Appli
2	1675	100.0	316	9 US-10-105-057-2	Sequence 2, Appli
3	1554	92.8	294	9 US-09-877-650-11	Sequence 11, Appl
4	1554	92.8	294	10 US-09-871-856-11	Sequence 11, Appl
5	1417.5	84.6	317	9 US-09-877-650-13	Sequence 13, Appl
6	1417.5	84.6	317	10 US-09-813-329-7	Sequence 7, Appli
7	1417.5	84.6	317	10 US-09-871-856-13	Sequence 13, Appl
8	1101	65.7	245	9 US-10-017-910-2	Sequence 2, Appli
9	855	51.0	160	9 US-09-779-050A-14	Sequence 14, Appl
10	768	45.9	160	9 US-09-779-050A-15	Sequence 15, Appl
11	496	29.6	109	10 US-09-911-777-8	Sequence 8, Appli
12	238.5	15.4	279	12 US-10-066-209-3	Sequence 3, Appli
13	238.5	15.4	281	8 US-08-916-625B-6	Sequence 6, Appli
14	238.5	15.4	281	8 US-08-971-317A-8	Sequence 8, Appli
15	238.5	15.4	281	9 US-10-001-054-54	Sequence 54, Appl
16	238.5	15.4	281	9 US-10-093-766-54	Sequence 54, Appl
17	238.5	15.4	281	9 US-10-174-654-11	Sequence 11, Appl
18	238.5	15.4	281	9 US-10-151-882-41	Sequence 41, Appl
19	238.5	15.4	281	10 US-09-813-329-17	Sequence 17, Appl

20	258.5	15.4	281	10 US-09-193-663-8	Sequence 8, Appli
21	258.5	15.4	281	10 US-09-934-465-1	Sequence 1, Appli
22	258.5	15.4	281	12 US-10-039-785-66	Sequence 66, Appl
23	258.5	15.4	281	12 US-10-011-125-4	Sequence 4, Appli
24	244	14.6	291	9 US-10-017-910-6	Sequence 6, Appli
25	234	14.0	296	9 US-10-185-425-5	Sequence 5, Appli
26	232	13.9	246	10 US-09-855-544A-13	Sequence 13, Appl
27	230.5	13.8	168	10 US-09-900-530A-10	Sequence 10, Appl
28	229.5	13.7	166	9 US-09-779-050A-16	Sequence 16, Appl
29	225	13.4	172	9 US-09-779-050A-17	Sequence 17, Appl
30	220.5	13.2	164	12 US-10-116-378-29	Sequence 29, Appl
31	183	10.9	278	10 US-09-246-129B-6	Sequence 6, Appli
32	183	10.9	278	10 US-09-899-059-6	Sequence 6, Appli
33	182	10.9	279	9 US-10-017-910-5	Sequence 5, Appli
34	181	10.8	279	8 US-08-971-317A-4	Sequence 4, Appli
35	181	10.8	279	10 US-09-193-663-4	Sequence 4, Appli
36	176	10.5	87	10 US-09-880-457-4	Sequence 4, Appli
37	176	10.5	94	10 US-09-880-457-5	Sequence 5, Appli
38	176	10.5	95	9 US-10-227-884-82	Sequence 82, Appl
39	176	10.5	95	9 US-10-230-163-82	Sequence 82, Appl
40	176	10.5	95	9 US-10-218-631-82	Sequence 82, Appl
41	176	10.5	95	9 US-10-230-338-82	Sequence 82, Appl
42	176	10.5	95	9 US-10-230-414-82	Sequence 82, Appl
43	176	10.5	95	9 US-10-216-159A-82	Sequence 82, Appl
44	176	10.5	95	10 US-09-880-457-6	Sequence 6, Appli
45	173.5	10.4	281	8 US-08-971-317A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-10-017-910-4
; Sequence 4, Application US/10017910
; Patent No. US20020159970A1

GENERAL INFORMATION:

APPLICANT: Choi, Yongwon
Wong, Brian
Josien, Regis
Steinman, Ralph

TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY

INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/447,035

FILING DATE: 1999-11-22

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-200

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

QY 143 PAMMEGSLDVAQRKPEAQPFALHTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 202
DB 121 PAMMEGSLDVAQRKPEAQPFALHTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 180
QY 203 GKLRVNDGFFYLYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
DB 181 GKLRVNDGFFYLYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240
QY 263 WSGNSEFHYFYSINVGGFFKLAGEEISIQVSNPDLDPDQDATYFGAFKVVQDID 316
DB 241 WSGNSEFHYFYSINVGGFFKLAGEEISIQVSNPDLDPDQDATYFGAFKVVQDID 294

RESULT 4

US-09-871-856-11
; Sequence 11, Application US/09871856
; Patent No. US20020081720A1
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent
Maraskovsky, Eugene

TITLE OF INVENTION: Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/871,856

FILING DATE: 31-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/996,139

FILING DATE: <Unknown>

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2851-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 294 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-871-856-11

Query Match 92.8%; Score 1554; DB 10; Length 294;
Best Local Similarity 99.7%; Pred. No. 4.5e-129;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPAPAPPAPPAASRSMFLALLGLGLGVVVCSTALFLYFRAQMDPNRISE 82
DB 1 GVPHEGLHPAPAPAPAPPAPPAASRSMFLALLGLGLGVVVCSTALFLYFRAQMDPNRISE 60
QY 83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGVQKELQHVGPQFSGA 142
DB 61 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGVQKELQHVGPQFSGA 120

QY 143 PAMMEGSLDVAQRKPEAQPFALHTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 202
DB 121 PAMMEGSLDVAQRKPEAQPFALHTINAASIPSGSHKVTLSWYHDSRWAKISNMTLSN 180
QY 203 GKLRVNDGFFYLYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 262
DB 181 GKLRVNDGFFYLYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN 240
QY 263 WSGNSEFHYFYSINVGGFFKLAGEEISIQVSNPDLDPDQDATYFGAFKVVQDID 316
DB 241 WSGNSEFHYFYSINVGGFFKLAGEEISIQVSNPDLDPDQDATYFGAFKVVQDID 294

RESULT 5

US-09-877-650-13
; Sequence 13, Application US/09877650
; Patent No. US20020169117A1
GENERAL INFORMATION:

APPLICANT: Anderson, Dirk M.

Galibert, Laurent
Maraskovsky, Eugene

TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation, Law Department

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Power Macintosh 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/877,650

FILING DATE: 08-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/995,659

FILING DATE: 1997-12-22

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2852-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 317 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-877-650-13

Query Match 84.6%; Score 1417.5; DB 9; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSEEMSGGVPHEGLHPAPAPAPPAPPAASRSMFLALLGLGLG 60
DB 1 MRRASRDYTKYLRSEEMSGGVPHEGLHPAPAPAPPAPPAASRSMFLALLGLGLG 59
QY 61 VVCSIALFLYFRAQMDPNRISEDTLPHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
DB 1 VVCSIALFLYFRAQMDPNRISEDTLPHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118

Db 60 VVCSVALLFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQTLTLESQDTKLIPDSCRR 119
Qy 119 KOAFQAVOKELQHVGPQFSGAPAMGEGSWLDVAORCKPEAOPFAHLLTINAAIPSGS 178
Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQOPFAHLLTINATDIPSGS 179
Qy 179 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLYANICFRHETSGSVPTDYLQIM 238
Db 180 HKVSLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLYANICFRHETSGDLATLQIM 239
Qy 239 VYVKTSTIKIPSSHNLKMGSTKWSGNSSEPHFYSINVGFFKLRAGEISIQVSNPSLL 298
Db 240 VYVKTSTIKIPSSHNLKMGSTKWSGNSSEPHFYSINVGFFKLRAGEISIEVSNPSLL 299
Qy 299 DPQDQATYFGAFKVDID 316
Db 300 DPQDQATYFGAFKVRDID 317

RESULT 6

US-09-813-329-7

Sequence 7, Application US/09813329

Patent No. US20020012968A1

GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-7

Query Match. 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYKYLRSSEEMSGGVPHEGLHPAPAPAPPPAASRSMFALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEEMSGGVPHEGLHPAPAPPPAASRSMFALLGLGLGQ 59
Qy 61 VVCSVALLFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQTLTLESQDTKLIPDSCRR 118
Db 60 VVCSVALLFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQTLTLESQDTKLIPDSCRR 119
Qy 119 KOAFQAVOKELQHVGPQFSGAPAMGEGSWLDVAORCKPEAOPFAHLLTINAAIPSGS 178
Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQOPFAHLLTINATDIPSGS 179
Qy 179 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLYANICFRHETSGSVPTDYLQIM 238
Db 180 HKVSLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLYANICFRHETSGDLATLQIM 239
Qy 239 VYVKTSTIKIPSSHNLKMGSTKWSGNSSEPHFYSINVGFFKLRAGEISIQVSNPSLL 298
Db 240 VYVKTSTIKIPSSHNLKMGSTKWSGNSSEPHFYSINVGFFKLRAGEISIEVSNPSLL 299
Qy 299 DPQDQATYFGAFKVDID 316
Db 300 DPQDQATYFGAFKVRDID 317

RESULT 7

US-09-871-856-13

Sequence 13, Application US/09871856

Patent No. US20020081720A1

GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER/READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/871,856
FILING DATE: 31-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,139
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-871-856-13

Query Match 84.6%; Score 1417.5; DB 10; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.2e-117;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYKYLRSSEEMSGGVPHEGLHPAPAPPPAASRSMFALLGLGLGQ 60
Db 1 MRRASRDYKYLRSSEEMSGGVPHEGLHPAPAPPPAASRSMFALLGLGLGQ 59
Qy 61 VVCSVALLFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQTLTLESQDTKLIPDSCRR 118
Db 60 VVCSVALLFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQTLTLESQDTKLIPDSCRR 119
Qy 119 KOAFQAVOKELQHVGPQFSGAPAMGEGSWLDVAORCKPEAOPFAHLLTINAAIPSGS 178
Db 120 KOAFQAVOKELQHVGSQHRAEKAMVDGSLDLAKRSKLEAQOPFAHLLTINATDIPSGS 179
Qy 179 HKVTLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLYANICFRHETSGSVPTDYLQIM 238
Db 180 HKVSLSSWYHGRGWAKISNMTLSNGLRVNODGFFYLYANICFRHETSGDLATLQIM 239
Qy 239 VYVKTSTIKIPSSHNLKMGSTKWSGNSSEPHFYSINVGFFKLRAGEISIQVSNPSLL 298
Db 240 VYVKTSTIKIPSSHNLKMGSTKWSGNSSEPHFYSINVGFFKLRAGEISIEVSNPSLL 299
Qy 299 DPQDQATYFGAFKVDID 316
Db 300 DPQDQATYFGAFKVRDID 317

RESULT 8
US-10-017-910-2
; Sequence 2, Application US/10017910
; Patent No. US20020159970A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Yongwon
; Wong, Brian
; Josien, Regis
; Steinman, Ralph
; TITLE OF INVENTION: A PROTEIN BELONGING TO THE TNF SUPERFAMILY
; INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAM
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/017,910
; FILING DATE: 14-Dec-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/447,035
; FILING DATE: 1999-11-22
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-017-910-2
Query Match 65.7%; Score 1101; DB 9; Length 245;
Best Local Similarity 84.1%; Pred. No. 2.7e-89;
Matches 206; Conservative 14; Mismatches 23; Indels 2; Gaps 1;
QY 74 QMDPNRISDSTGTCFYRLRLHFNAGLDSTLESDT--LPDSRRMKQAFQAVQKELQ 131
Db 1 QMDPNRISDSTGTCFYRLRLHFNAGLDSTLESDT--LPDSRRMKQAFQAVQKELQ 60
QY 132 HVGQPFQSGAPNMGCSWLDVAQGRPEAQPFAHLTINAAIPSGSHKVTLSWYHNRG 191
Db 61 HVGQSHIRAEKAVQSGWLDLAKRSKLEAQPFAHLTINAAIPSGSHKVTLSWYHNRG 120
QY 192 WAKLSNNTLSNGLRVNQDGFYILYANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSS 251
Db 121 WGLSNMTFNGKLIVNQDGFYILYANICFRHHETSGDLATEYLQVMVYVVKTSIKIPSS 180
QY 252 HNLKMGSTKNWGSNPFHYSINVGGFFKLRAAGEEISIQVSNPDLDPDQDATYFGAFK 311
Db 181 HTLMKGGSTKYWSNPFHYSINVGGFFKLRSCEEISIEVSNPDLDPDQDATYFGAFK 240
QY 312 VQDID 316
Db 241 VRDID 245

RESULT 9
US-09-779-050A-14
; Sequence 14, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-14
Query Match 51.0%; Score 855; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 7e-68;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 157 GKPEAOPFAHLTINAAIPSGSHKVTLSWYHNRGWAHAKISNMTLSNGLRVNQDGFYLY 216
Db 1 GKPEAOPFAHLTINAAIPSGSHKVTLSWYHNRGWAHAKISNMTLSNGLRVNQDGFYLY 60
QY 217 ANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKNWGSNPFHYSINV 276
Db 61 ANICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKNWGSNPFHYSINV 120
QY 277 GGFKLRAGEEISIQVSNPDLDPDQDATYFGAFKVQDID 316
Db 121 GGFKLRAGEEISIQVSNPDLDPDQDATYFGAFKVQDID 160
RESULT 10
US-09-779-050A-15
; Sequence 15, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-15
Query Match 45.9%; Score 768; DB 9; Length 160;
Best Local Similarity 89.9%; Pred. No. 3.2e-60;
Matches 143; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
QY 158 KPEAOPFAHLTINAAIPSGSHKVTLSWYHNRGWAHAKISNMTLSNGLRVNQDGFYLYA 217
Db 2 KLEAOPFAHLTINATDIPSGSHKVTLSWYHNRGWAHAKISNMTFNGKLIVNQDGFYLYA 61
QY 218 NICFRHHETSGSVPTDYQLQVMVYVVKTSIKIPSSHNLKMGSTKNWGSNPFHYSINV 277
Db 62 NICFRHHETSGDLATEYLQVMVYVVKTSIKIPSSHTLMKGGSTKYWSNPFHYSINV 121

;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100263
;; PRIOR FILING DATE: 1998-09-14
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/101476
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/107783
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112420
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/116533
;; PRIOR FILING DATE: 1999-01-20
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/131294
;; PRIOR FILING DATE: 1999-04-07
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/162506
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: 60/170262
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/187202
;; PRIOR FILING DATE: 2000-03-03
;; PRIOR APPLICATION NUMBER: 60/209832
;; PRIOR FILING DATE: 2000-06-05
;; PRIOR APPLICATION NUMBER: 60/232887
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/218517
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 09/284291
;; PRIOR FILING DATE: 1999-04-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380913
;; PRIOR FILING DATE: 1999-09-09
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/866034
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/882636
;; PRIOR FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/924419
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: PCT/US98/18824
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/US99/00106
;; PRIOR FILING DATE: 1999-01-05
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/08615
;; PRIOR FILING DATE: 1999-04-20
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28634
;; PRIOR FILING DATE: 1999-12-01
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00376
;; PRIOR FILING DATE: 2000-01-06
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04342
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/06884
;; PRIOR FILING DATE: 2000-03-15
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: PCT/US00/13705
;; PRIOR FILING DATE: 2000-05-17
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/14941
;; PRIOR FILING DATE: 2000-05-30
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/22031
;; PRIOR FILING DATE: 2000-08-11
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/06666
;; PRIOR FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: PCT/US01/17092
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29

;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: PCT/US01/27099
;; PRIOR FILING DATE: 2001-08-29
;; NUMBER OF SEQ ID NOS: 91
;; SEQ ID NO 54
;; LENGTH: 281
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match 15.48; Score 258.5; DB 9; Length 281;
Best Local Similarity 26.48; Pred. No. 5e-15; Indels 51; Gaps 10;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;

Qy	43	PAASRSMFLALIGLIGQVVGCSIALFLYFRAQMD--PNRISEDSHCHFYRILRLHENAGL	100
Db	10	PSLGQTCVLIYFTVLQSLCAVYVYFTNELKQMDKYSKGIACF-----LKEDDSY	64
y	101	QDSTLESDTLPDSCRRMKQAFQGAQVK-----ELQHVGPQRFSGAPAMM	146
Db	65	WDP--NDESNMSPCQWKQLRQLVRKMLRTSEETISTVQEKQONISPL-----	113
Qy	147	EGSWLDVAQRGKPEAQPFahlT-----INAAIPSGSHKVTL-----SSWYHDR-GWAKIS	196
Db	114	-----VRERGQRVA--AHITGTRGNTLSSPNKNEKALGRKINSWESSRSGHSFLS	165
Qy	197	NMTLSNGKLRVNDGFFYLXANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK	256
Db	166	NHLRNGELVHEKGFYIYSQTYFRQEEIKENTKNDKQWQYIYKYT-SYDPDILLMK	224
Qy	257	GGSTKNWGSNSEFFHYSINVGGFFKLRAEEISIQVSNPSLLDPDODATYFGAKV	312
Db	225	SARNSCWKSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDBEASFCAFLV	280

Search completed: April 16, 2003, 12:21:52
Job time : 15.5 secs